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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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2: pir2:*
3: pir3:*
4: pir4:*
    MLLRSKPALPPPLMLLLLGP.....LPAFSYSFFVIRNAKVAACI 543
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hypothetical prote beta-xylosidase [i probable fimbrial microtubule-associ phosphoribosylamin adenylosuccinate s probable peptidogl beta-fructofuranos transcription anti retrotransposon li transketolase [imp hypothetical prote methionyl-trNA syn DNA gyrase subunit toxin secretion AB conserved hypothet endo-1,4-beta-xyla dynein heavy chain dynein heavy chain
                                                                                                                                                                                                                                                                                                                     hypothetical prote hypothetical prote beta-fructofuranos hypothetical prote hypothetical prote hypothetical prote hypothetical prote probable outer mem
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B 8	Db Qy	Qy Db	Db Qy	망왕	Db Qy	망왕	Query Ma Best Loc Matches	RESULT 1 JC7506 heparanase C;Species: C;Date: 17-7 C;Accession R;MCKenzie, Biochem. Bio A;Title: Cil A;Title: Cil A;Reference A;Reference A;Residues: A;Residues: A;Cross-ref C;Comment: therapies. C;Gene: hps: A;Map posit. C;Keywords:		C C C C C C C C C C C C C C C C C C C
351 GJ 277 G	291 DS : 217 DA	232 KJ 157 MI	172 VI 149	112 FI 136	56 FJ 78 FJ	20 PJ 18 PJ	tch als 202	ESULT 1 C7506 eparanase prote ; Species: Homo ; Date: 17-Nov-; ; Accession: JC; ; Accession: JC; ; Accession: JC; ; Accession: JC; ; Molecule type ; Molecule type ; Molecule type ; Residues: 1-4; ; Cross-reference ; Croment: This herapies. ; Genetics:		98.5 98.5 98.5 98.5 98.5 98.5 98.5 98.5
APLLSDTF) :: NNLSDSY)	SVTWHHYYI	KADIFINGS(; MHGRAVNGS(TTFANCS	BERSYWQS	SVTIDANI	PLGPLSPGAL : PPACLAPGAL	imilarity ; Conservat	protein 2a - human low- sapiens (man low-2000 #sequency JC7506 E.; Tyson, K.; Si phys. Res. Commun ning and express. JC7506 JC		ָט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט ט
AAGFMWL : AAGFLWL	LNGRTAT :: IDGRVVK	INGSQLGEDYIQLHKLLRK- : vNGSQLGKDYIQLKSLLQPI	3LDLIFG	QVNQDIC	LATDPRF:	P	31.6%; 36.0%; vative	human (man)		596 629 654 659 701 746 1012 1612 1612 1613 716 716 811 454
HTL HTL	RED 	27 17 17 17 17	LNA	KY	LDF	STH		rev mps 27 n p n p		0000000000000000
GLSARMGIEVVMRQVFFGAG : : mlanqgidvvirhsffdhg	DSVTWHYYLNGRTATREDFLNPDVLDIFISSVQKVFQVVE :	KLLRK-STFKNAKLYGPDVG : :: SLLQPIRIYSRASLYGPNIG	LLRTADLQWNSSNAQLLLDY	GGPGPDGGPGPD	LSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIF 		Score 897.5; DB 2; Pred. No. 9.2e-59; 4; Mismatches 146;	RESULT 1 UC7506 heparanase protein 2a - human C;Species: Homo sapiens (man) C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change C;Accession: JC7506 R;McKenzie, E.; Tyson, K.; Stamps, A.; Smith, P.; Turner, P.; B Biochem. Biophys. Res. Commun. 276, 1170-1177, 2000 A;Title: Cloning and expression profiling of Hpa2, a novel mamm A;Reference number: JC7506 A;Molecule type: mRNA A;Residues: 1-480 <mck> A;Cross-references: UNJPROT: (99HB39; GB:AF282885 C;Comment: This protein, a intracellular membrane-bound enzyme, C;Genetics: A;Genetics: A;Genetics: hpa2a A;Map position: 10q23-10q24 C;Keywords: heparin binding; membrane bound</mck>	ALIGNMENTS	T04506 C64180 C64180 P951202 D98014 D98014 D98014 D98010 D98010 D98010 D98010 D98010 D98010 JC5925 T19113 T19113 T19113 C10103 C10106 D98010 JC5925 J
GAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLF 410 :: : : : :	DSVTWHHYYLNGRTATREDFLNÞDVLDIFISSVQKVFQVVESTRÞGKKVWLGETSSAYGG 350 : ::	KADIFINGSQLGEDYIQLHKLLRK-STFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVI 290 	VLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEBNSFLK 231 : 	EERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD 171 	LSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKEST 111	LGPLSPGAL	Length 480; Indels 139; Gaps 9;	2000 #text_change 09-Jul-2004 P.; Turner, P.; Barry, R.; Hircock, M.; Pa 2000 pa2, a novel mammalian heparanase family m 5 ane-bound enzyme, has biological and thera		hypothetical prote hypothetical prote NADH2 dehydrogenas DNA topoisomerase DNA topoisomerase siderophore recept RhtA Rhizobactin r membrane klotho pr hypothetical prote RNA-directed RNA p hypothetical prote probable membrane probable membrane probable membrane probable membrane probable membrane probable membrane probable DNA gyras

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A; Note:
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A;Residues: 1-521 <BEV>
A;Cross-references: UNIPROT:Q9SDA1; EMBL:;
A;Experimental source: cultivar Columbia;
C;Genetics:
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T45608
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A; Accession: T45608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 04-Feb-2000
C;Accession: T45608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F13G24.30 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;Map position: 5
.;Introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
.;Note: F13G24.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154;
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                          NGKSLKPTATGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFDASAC 520
                                                                NGLTLKMVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC 542
                                                                                                                                                                                         ALLWHRLMGKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLLINLSNQSDFTVS
                                                                                                                                                                                                                               SLLFKKLVGTKVLMASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                          YNSGGRHVSDŤĖIDSĖWYĹDQĹĊMŚARHNTKVYCRQTLVG-ĠFYGĹLEKGTĖVĖNĖDÝYS
                                                                                                                                                                                                                                                                                                                YGGGAPLLSDTFAAGFWWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDB-NFDPLPDYWL 406
                                                                                                                                                                                                                                                                                                                                                           THHIYNLGSGNDPALVKKIMDPS----YLSQVSKTFKDVNQTIQEHGPWASPWVGESGGA
                                                                                                                                                                                                                                                                                                                                                                                                 TWHHYYLNGRT--ATREDFLNPDVLDIFISSYQKVF----QVVESTRPGKKVWLGETBSA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                           AELYGKDLIVLKDVINK-VYKNSWLHKPILVAPGGFYEQQWYTKLLEI---SGPSVVDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSQLGEDYIQLHKLLRKSTFKNAKLYGPDVGQP-----RRKTAKMLKSFLKAGGEVIDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLNALRGRHKLRGKAWGGAWDHINTODFLNYTVSKGYVIDSWEFGNELSG--SGVGASVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLNALLRTADLQ------WNSSNAQLLLDYCSSKGYNI-SWELGNEENSFLKKADIFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTRPLLTKAIKAFKPLRIRIGGSLQDQVIYDVGNLKT-----PCR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVIPPVTMGFFVVKNVNALAC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYLRLPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSS 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKLVGTKVLMASVQGSKRR-------KLRVYLHCTNTDNPRYKEGDLTLYAINLHNVT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --PFQKM-----NSGLFGFSKGCLHMKRWDELNSFLTATGAVVTF
                                                                                                                                                 -----RLPYPFS---NKQVDKYLLRP---LGPHG--LLSKSVQL 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 416; DB 2; 29.2%; Pred. No. 5.8e-23;
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                                                                                                                                                                            A; Map position: REV596956-595886
                                                                                                                                                                                                                  A; Cross-references: UNIPROT: Q58084;
                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type; DNA A;Residues; 1-356 <BUL>
                                                                                                                                                                                                                                                                                                     C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 (;Accession: F64383 R;Bult, C.J.; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A., rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschii A;Accession: F64383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein MJ0670 - Methanococcus jannaschii
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A;Note: T2L5.6
C;Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6
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A;Experimental source: cultivar Columbia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-190 <GEI>
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126 ICKY-----GSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 YSFFVIRNAKVAAC 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441 DNPRYKEGDLTILYAINLHNV-------TKYLRLPYPPSNKQVDKYLLRPL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382 RQVFFGAGNYHLVD-ENFDPLPDYWLSILFKKLVGTKVLMASVQGSKRRKLRVYLHCTNT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 ---ROSKG-ITVLLMNLDNTTTVVAKVELNNSFSLRHTKHMK-----SYKRASSQLFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPHGLL------$KSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RÓSLIG-GNYGLLNTTNÉTÉNPDYYSALIWROLMGRKALFTTESGTK--KIRSYTHCA--
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.0%; Score 169.5; DB 2;
ilarity 27.8%; Pred. No. 2.5e-05;
Conservative 34; Mismatches 57;
                                                                                       4.0%;
                                                              48; Mismatches 143;
                                                                                     Score 112.5;
Pred. No. 1.1;
                                                                                                                                                                                                                  GB:U67514;
                                                                                                                                                                                                     GB:L77117; NID:g2826304; PIDN:AAB98664.1;
                                                                                                       DB 2;
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                                                              Indels 125;
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beta-fructofuranosidase (EC 3.2.1.26) - fava bean C;Species: Vicia faba (fava bean) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change C;Accession: T12094 R;Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U. Plant Cell 7, 1835-1846, 1995 Plant Cell 7, 1835-1846, 1995 A;Title: Seed coat-associated invertases of Fava bean control bo A;Reference number: Z17416; MUID:96093423; PMID:8535137 A;Accession: T12094
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C;Superfamily: beta-fructofuranosidase
C;Keywords: cell wall; glycoprotein; glycosidase; hydrolase
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A;Experimental source: cv. Fribo, seed coat
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       GQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRT 304
                                             TLA----
                                                                               KKADIFINGSQLGEDYIQL-----HKLL----RKSTFKNAKLYGP------DV
                                                                                                                                                        DVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFL
                                                                                                                                                                                                DDVKKGWAGIQAIPRTVWLDSSRRQLR-QWPVEELNRLRGKQVEMKNRKLKKGGY----L
                                                                                                                                                                                                                                  DICKYG-----SIPPDV-----EEKLRLEWPYQEQLLLR----EHYQKKFKNSTYSRSSV 170
                                                                                                                                                                                                                                                                        TYLONODKYIPDKTSEDGWGGLRYDYGNFYASKSFFDPTK----NRRIIWGWANESDTKE
                                                                                                                                                                                                                                                                                                             AYLR------PGGTKTDF-----LIFDPKKESTFEERSYW----QSQVNQ 124
                                                                                                                                                                                                                                                                                                                                                   KHPIHSAKRTGMWECPDFYPVSLEGKNGLD--LSMMMGNNVKHVLKNSLDITRYEYYTIG
                                                                                                                                                                                                                                                                                                                                                                                       QEPLHLVS-----PSFLSVTIDANLATDPRFLILLGSPKLRTLARGLS-----P
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                                                                                                                     EVKGITASQADVEVTFSFSSLDKAEAFDPNWENAE---DLCAQKGSKVRGGVG--PFGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                         3.9%; Score 111.5; DB 2; ilarity 21.4%; Pred. No. 2.7; Conservative 48; Mismatches 107;
                                           SKKLEEYTSVFFRVFKAANKHKILMCSDAKSSSLNRELYKPSFAGFVNVDL
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RESULT 7
$32961
hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 4
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skbl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F6E21.40 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T10666
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A; Residues: 1-670 < BEV >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z16533
A; Accession: T10666
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                                                                                                                                                          524 LPAFSYSFFV 533
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                                                                                                                                                                                                RFWNAPEQADILVSELLGSFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDYCSSKGYNISWELGN-----EPNSFLKKA-DIFIN-----GSQLGEDYIQLHKLL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVLRMDSETTLKQEIAWATHLSLQMCB-----PD------LTRPHYLAGGL 139
                                                                                                                       IPS-SYTSFI
                                                                                                                                                                                                                                      PFSN--KQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLM---EKPLRPGSSLG 523
                                                                                                                                                                                                                                                                          RASLQAAEETDRKLKVY - - - AVEKNPN - -
                                                                                                                                                                                                                                                                                                       -ASVQGSKR--RKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTK------YLRLPY
                                                                                                                                                                                                                                                                                                                                                 ---RDSVKYIQYQ---RAVEKALVDR----VPDEKASEL----TTVLMVVGAGRGPLV
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                                                                                                                                                                                                                                                                                                                                                                                       LSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM------
                                                                                                                                                                                                                                                                                                                                                                                                                              KNP--LRIYLDYVAYLFQKMESLSEQERIELGYRDFLQAPLQPLMDNLEAQTYETFE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD--TSEGLNDSWELWNSFRLLCEHDSKLSVALDVLSTLPSETSLGRWMGES-VRAAILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KESTFBERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -GYPCLSKRHQKLIAGFFDHAAQVVICGKPVHNLQKPLDSSSEGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 111; DB; Pred. No. 3.7; 77; Mismatches
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                                                                                                                                                                                                                                                                          -AVVTLHNLVKMEGWEDVVTIISCDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194; Indels 156;
                                                                                                                                                                                                -DNELSPECIDGAQRFIKP-DGIS
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A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-2298 <SCH>
A;Cross-references: UNIPROT:Q96U00; EMBL:AL355933; Gs
A;Cross-references: BAC clone B8B20; strain OR74A
C;Genetics:
A;Gene: NCSP:B8B20.20
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
T49648
                                                                                   A; Map posit
A; Introns:
                                                                                                                                                                                                                                                                                                    R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, I submitted to the Protein Sequence Database, May
                                                                                                                                                                                                                                                                                                                                                             hypothetical protein B8B20.20 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                   A; Accession: T49648
                                                                                                                                                                                                                                                                                    A; Reference number: 225022
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A;Reference number: S45940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast 9, 189-199, 1993
A;Title: The complete sequence of a 19,482 bp segment located
A:Reference number: S29348; MUID:93220397; PMID:8465606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S32961; S46140
R;Doignon, F: Biteau, N.; Crouzet, M.; Aigle, M.
Yeast 9, 189-199, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-688 < AIG>
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;Map position: 2R
    Matches
                           Best Local
                                              Query Match
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                                                                                                        position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 ICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSS-----VDVLYT 175
                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVKDFHIQVIKYLNSOFKNNYSTLMTSSKTQDRRKSHNMPSSILDDGNKIGMHVSPIDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDFAHIRSLKWDSNDKVESLIRALIFNDMFPYFNKEQVDTKADGIFFLRLLRKNFKEHIN 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAEYSSWKWDSDDKRQLQFMYEFRMKLKECLVKFYENFDLQKSSDPLKELIIPWEKIVYV 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YSHFIDNDEPLWRDKVYPKIYTNEQTPTPDASAIFDS--HKIYAIISLLRYYLPEKR 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ANC--IDAFTGEQVRIDGAELIWTSKNLVFSSISSAVLRLNDLQNMFSAFRPYGEEALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NISWELGNEPNSFLKKA---DIF--INGSQLG--EDYIQLHKLLRK-----
    Conservative
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3.9%; Score 111; DE 19.3%; Pred. No. 24; tive 79; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RTATREDFLNPDVLDIFISSVQKVFQVVESTR----PGKK 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Mismatches
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                                                                                                                                                                                                                                                                                                                              Brandt, P.;
                                           BB
  190;
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                                                                                                                                                                                   GSPDB:GN00116;
                                                                                                                                                                                                                                                                                                                       Fartmann,
                                         Length 2298;
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    Indels
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    208;
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    Gaps
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    28;
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RESULT
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-879 < HAY>
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                                                                                                                                   Genetics:
                                                                                       Query Match
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                                                                       Similarity
                          VSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKEST
MSGSYVNAWAENEIQFDSRFLELKGDTKI-DLKRFSSQGYVEPG--KYNLQVQLNKQPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AS-LDVLKQAKTLEAAIYTLNVTQLQKMCTTLHFGSPGFDWGILNVAL-----DTHAHFL 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYMSAESDIEQQFRALSAENMRSIDAAWREELITKN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----DOTLPPLMEKPLRPG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLKAITTFGKQTEQVACTEKTVTLAAKLAAR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWIETSSEEQYSSNESSADIDPRQLEDAILLLQEKLTKEFFWMA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSGLDLIFGLNAL-----LRTADLQ------WNSSNAQLLLDYCSSKGYNI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYGSIPPDVEEKLR-----LEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFAN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------MASVQGSK-----RRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K------KVWLGETSSAYGGGAPLLSDTFAAG-----FMWLDK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKLRTLARGLSPA----
                                                           Conservative
                                                                       3.9%;
                                                        68;
                                                         Score 109.5; I
Pred. No. 7.3;
68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YLRFGGTKTDFLIFDPKKESTFEERSYWQSQV-NQDIC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SSLGLPAFSYSF-FVIRNAKVA 540
                                                                       .
3
                                                                                     DB
                                                         208;
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    Escherichia coli (strain

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                                                         Indels
                                                                                     Length
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                                                         241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RELLAL
                                                                                                                                                                                                                                                         coli 0157:H7
                                                         Gaps
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112 FEERSYWQSQVNQDICKYGSIPPDVEEKL-----RLEWPYQEQLLLREHYQKKFKNS

EEYDIYWYASENDASKTYACLTPELVAQFGLKEDVAKNLQWIHDGKCLKPGQLE-----

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RESULT 10
874760
hypothetical protein slr1617 - Synechocystis sp. (strain PCC 6803)
c; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: 874760
C; Accession: 874760
C; Accession: 874760
C; Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; C; Kaneko, T.; Sato, S.; Simpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda O, K.; Okumura, S.; Simpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda Res. 3, 109-136, 1996
DNA Res. 3, 109-136, 1996
                                                                                                                   문
                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-411 <KAN>
A;Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA1691
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: S74322; MUID:97061201; A;Accession: S74760
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                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                       245
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                         261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVYISLSMPWGDSSTISY----NGNYGSGSDSSQVG--YFSRVDDAT 616
                                                                  DYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRT 304
                                                                                                                                                                      LLDYCSSKG----YNISWEL------GNEPNSFLKK-----ADIFINGSQLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQVQEYDINTASMPF----LTRPGQVRYKLMMGRPQEWGHHVEGGFF8GGEASWGIANGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQPRRKTAKMLKSFLKAGGEVI------
                       DHCRRTRGLRCAILRSSPVYGSMSDKP-----KFIFNFFKKASQGQKIVT--HHYING--
                                                                                                                                                                                                                    EFRLISPTREQIDI --- FAGSTKLDLLASEENIDCIVHLANPRVYTSNVAMGQTLTMLRN
                                                                                                                                                                                                                                                                     KFKNSTYSRSSVDVLYTFANCSGLDLIF---GLNALLRTADLQWNSSNAQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --YLRLPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFRDAGVSVYLNYTRHTYWDRDEQTNYNVMLSHYFNLGSIRNMSISMTGYRYEYDNQADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRRKLRVYLHCTNTDNPRYKEGDLTLYAI -----NLHNVTK----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSYSKDFDELNSRVTFAG---YRFSEENFMTMSEY-LDASDSEMVRTGNDKEMYTATYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI----EVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGT---KVLMASVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLYGGA---LADEHYQSAALGVGRDLSVFGAVAFDITHSHTRLDKETAYGKGSLDGNSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAYGGGAPLLSD-----GLSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDVLDIFISSVQKVFQVVESTRPGK---KVWL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGVAHTTAKVTVSQL---GRVIYETQVPAGPFRIQDLGDSV-----SGTLHIRIEEQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYAWRALPSIKAKIGIGEDY-----LNSDIFDGFNYVGGSISTDDQMLPPNIRGYAPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHEENGGDDSNEISGNGTVGVNLGAWRLRADWQTDYLHSKSNDDDVINGDDTQKNWEWSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYSRSSVDVLYTFANCSGLDLIFGL-NALLRTADLQWNSSN-----AQLLLDYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GIDIK---ADLSQSALVISLPQAYLEYTDINWDPPSRWDDGISGLIADYSITAQT
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                          21.4%;
                                                                                                                                                                                                                                                                                                                   3.8%; Score 108.5; 1
21.4%; Pred. No. 2.7;
ive 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SSKGYNI-SWEL-GNEPNSFL---KKADIFINGSQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGEDYIQLHKLLRKSTF------KNAKLYGPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -DSVTWHHYYLNGRTATREDFLN
                                                                                                                                                                                                                                                                                                                                                                 Length 411;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                     Gaps
                       311
                                                                                                                                                                      244
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                                                                                                                        260
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A; Residues: 1-500 <STO>
A; Cross-references: UNIP;
C; Genetics:
A; Gene: CC2357
                 A;Molecule type: DNA
A;Residues: 1-879 <TO:
A;Cross-references: UNIPROT:Q8XCP4; GB:AE005174; NID:g12516702; PIDN:AAG57466.1;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                       A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: F85875 A;Status: preliminary
                                                                                                                                                                                                                                        probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: F85875
C;Accession: F85875
R;Perna, N.T.; Plunkett III, G; Burland, V.; Mau, B.; Glasner, J.D.; Rose, |
R;Perna, N.T.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, |
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, |
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87541
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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nes 56; Conserv
Z3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKAIDPSLRVGGPATAGAAWVPEFLAHVKKSGSAVDFVTTHTYGVDGGFLDEKGVQDTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHHLRARYGVEEVRTWFFEVWNEPNLDGFWEKAD-----QAAYFELYDV----TARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSRSSVDVLYTFANCSGLDLIFGLN---ALLRTAD---LQW--NSSNAQL-----LLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGFMWLDKLGLSA-----RMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPDVLDIFISSVQKVFQVVE-STRPGKKVWLGETSSAY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -YCSSKGYNI----SW--ELGNEPN--SFLKKADIFINGSQLGEDYIQLHKLLRKSTFKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKSLLHQI 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPSP-DAVVGDVRRVREQIEASAFPGLPLYFTEWSTSY 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKLYGPD--VGQPRRKTAKMLKSFL---KAGGEVIDSVTWHHYYLNG----RTATREDFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YDWTKIDQLYDALLAKGIKPFIELGFTPEAMKTSDQTIFYWKGNTSHPKLGPWRDLIDAF 140
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25.7%;
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K.; Apodaca,
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-670 <YAM>
                                                                                            A;Residues: 1-670 <MCD>
A;Cross-references: UNITROT:042667; EMBL:AL009227;
A;Experimental source: strain 972h-; cosmid c27D7
R;Yamashita, A.; Watanabe, Y.; Yamamoto, M.
Genes to Cells 2, 155-166, 1997
                                                                                                                                                                                                                                 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: 73846; 700012
R;McDougall, R.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
                                               A;Title: Microtubule-associated coiled-coil A;Reference number: Z14042; MUID:97311255; A;Accession: T00012
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-670 < M
                                                                                                                                                                                                            A; Reference number: Z21793
A; Accession: T38446
                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                   microtubule-associated protein ssm4 - fission yeast (Schizosaccharomyces pombe)
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                          474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 NFRDAGVSVYLNYTRHTYWDRDEQTNYNVML---SHYFNLGSIRNMSISMTGYRYEYDN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427
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                                                                                                                                                                                                                                                                                                                                                                                                                                     QVDK----YLLRPLGPHGLLSKSVQLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSYSKDFDELNSKYTFAG---YRFSEENFMTMSEY-LDASDSEMVRTGNDKEMYTATYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI-----EVVMRQVFFGAGNYHLVDENFDDYBLDDYBLSLLFKKLVGT----KVLMASVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLYGGA---LADEHYQSAALGVGRDLSVFGAVAFDITHSHTRLDKETAYGKGSLDGNSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAYGGGAPLLSD------GLSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQVQEYDINTASMPF----LTRPGQVRYKLMMGRPQEWGHHVEGGFFSGGEASWGIANGW
                                                                                                                                                                                                                                                                                                                                                                                                        QADKGVYISLXMPWGD----SSTISYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRL------PYPFSNK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVAHTTAKVTVŠQL---GRVIYETQVPAGPFRIQDLGDSV----SGTLHIRIEEQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GOPRRKTAKMLKSFLKAGGEVI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYAWRALPSIKAKIGIGEDY-----LNSDIFDGFNYVGGSISTDDQMLPPNLRGYAPDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHEENGGDDSNEISGNGTVGVNXGAWRLRADWQTDYLHSKSNDDDVINGDDTQKNWEWSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYSRSSVDVLYTFANCSGLDLIFGL-NALLRTADLQWNSSN-----AQLLLDYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GIDIK----ADLSQSALVISLPQAYLEYTDINWDPPSRWDDGISGLIADYSITAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEYDIYWYASENDASKTYACLTPELVAQFGLKEDVAKNLQWIHDGKCLKPGQLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEERSYWQSQVNQDICKYGSIPPDVEEKL-----RLEWPYQEQLLLREHYQKKFKNS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSGSYVNAWAENEIQFDSRFLELKGDTKI-DLKRFSSQGYVEPG--KYNLQVQLNKQPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKEST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 106; D
Pred. No. 13;
                                                           PMID:9167972
                                                                                                                                                                                                                                                                                                                                                                                                        595
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                                                                                                                                        PIDN:CAA15832.1;
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
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Best Local
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80; Conser
                                                                                                                                                                                                                                                                                                                       RSSVDVLYTFANCSGLD-LIFGLNALLRTADLQWNSSNAQLL-LDYCSSKGYNISWELGN
SNNSSVDGVKTRR 408
                             VLMASVQGSKRRK
                                                                              GFMWLDKLGLSARMGIEVVMRQVFFGAGN----YHLVDENFDPLPDYWLSLLFKKLVGTK 417
                                                                                                                  PKSQDNWTTQVTPSSLLGVSEVSKVLQL
                                                                                                                                          ATREDFLNPDVLD---IFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFAA 361
                                                     -LVKIPKNPFSEKLTISNVNRYLNIVPGSLDLQFSLTNENF----VHWNSTVYQELLNLK 395
                                                                                                                                                                        FLRSK----NSIEKPRNFRREKFLKKFLAMQKEIKYLRKRKLQIRKIPNYKYSDRSLNSKT
                                                                                                                                                                                                       FKNAKLYGPDVGQPRR-KTAKMLKSFLKAGGEV-----IDSVTWHHYYLNGRT
                                                                                                                                                                                                                                VLQECEKKFTPHSKGSYLKENLKSELRKGRLDELMCENTALKEKIDKLNKELEKVEPQLT
                                                                                                                                                                                                                                                                                          KTA--TFYTSSTTENLDELNFSTEELSSFDTTLLNSDTSKLSGLDDSSFMEEEFVWQVDN
                                                                                                                                                                                                                                                                                                                                                                                 KKESTFEERSYWQSQVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYS 166
                                                                                                                                                                                                                                                           ------EPNSFLKK-----ADIFINGSQLGEDYIQLHKLLRK----ST
                                                                                                                                                                                                                                                                                                                                                      KRPSVVKSR----KKGSENISNFMEKTKAIKQKSRREPSKFERSLARPLCITPIDSSTPT
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                             430
                                                                                                                                                                                                                                                                                                                                                                                                                  58; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 105; D
Pred. No. 10;
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C;Date: 07-Sep-1990 #sequence revision 28-Oct-1994 #text_change 09-Jul-2004 (;Accession: S00652; T40496; T40422 R;MCKenzie, R.; Schuchert, P.; Kilbey, B. Curr. Genet. 12, 591-597, 1987 A;Title: Sequence of the bifunctional adel gene in the purine biosynthetic 1 A;Reference number: S00652; MUID:89003164; PMID:3502942 A;Accession: S00652 A;Access phosphoribosylamine-glycine ligase (EC 6.3.4.13) - fission yeast (Schizosaccharomyces pon N;Alternate names: AIRSase; aminoimidazole ribotide synthetase; GARSase; glycinamide ribotic synthetase; glycinamide ribotic synthetase; ghosphoribosylamine-glycine ligase (EC 6.3.4.13); phosphoribosylformylglycine C;Species: Schizosaccharomyces pombe

pathway

of the

A;Cross-references: UNIPROT:P20772; EMBL:X06601; NID:g4903; PIDN:CAA29820.1; PID:g4904 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A. submitted to the EMBL Data Library, February 1998 A;Reference number: Z21910 A;Accession: T40496

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-788 < WOO> A; Molecule type: DNA

A;Cross-references: EMBL:AL021730; PIDN:CAA16823.1; GSPDB:GN00067; SPDB:SPBC4C3.02c A;Experimental source: strain 972h-; cosmid c4C3 R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, March 1999

A;Reference number: Z21928 A;Accession: T40422

A;Status: preliminary; translated from GB/EMBL/DDB:

A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 604-788 <SEE>
A;Cross-references: EMBL:AL035655; PIDN:CAB38600.1; GSPDB:GN00067; SPDB:SPBC405.01
A;Cross-references: Strain 972h-; cosmid c405

109 112 112 154 165 199 221	15 LLLLGPLGPLSPGALPRPAQAQDVVDLD	\$ 4 \$ 4 \$ 4 \$ 4
09-Jul-2004 x, A.L.; Graham, D.E.; O Aquifex aeolicus. tion not shown PIDN:AAC07286.1; PID:929	ccinate synthetase - Aquifex acolicus : Aquifex acolicus 8-May-1998 #sequence_revision 08-May-1998 #text_change 0n: F70411 , G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox 2, 353-358, 1998 2, 353-358, 1998 2, 353-358, 1998 ce number: A70300; MUID:98196666; PMID:9537320 on: F70411 preliminary; nucleic acid sequence not shown; translate ctype: DNA eferences: UNF> eferences: UNFOT:067321; GB:AE000733; NID:g2983720; P eental source: strain VF5 senial source: strain VF5 mily: adenylosuccinate synthase mily: gcore 104; DB 2; Length 432; cal Similarity 23.9%; Pred. No. 6.4; 96; Conservative 39; Mismatches 128; Indels 1	adenylosuccina c;Species: Aqu C;Date: 08-May C;Accession: F R;Deckert, G:; V V Ature 392, 35 A;Title: The c A;Reference nu A;Accession: Fref A;Status: pref A;Residues: 1- A;Cross-refere A;Experimental C;Genetics: purA C;Superfamily: Query Match Best Local S Matches 96
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h 788; s 33; Gaps 11; www.getssay 348; ; ; ablggfggfelkQ 483 yhthosypelp 402 : : : : 1 1 1 1	3.7%; Score 104.5; DB 1; Lengt Similarity 27.7%; Pred. No. 15; Onservative 36; Mismatches 114; Indel 10; Conservative 36; Mismatches 114; Indel	Query Match Best Local Matches 7 Qy 297 Qy 424 Qy 349 Qy 348
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Q71rpl 'rattus norv
Q9qzf8 rattus norv
Q9qxf8 rattus spien
Q8wwq2 homo sapien
Q8wwq1 homo sapien
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Q8hb39 homo sapien
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Q8ff10 arabidopsis
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ALIGNMENTS

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A Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Atzmon R.,
A Ishai-Michaeli R., Bitan M., Pappo O., Peretz T., Michal I.
Spector I., Pecker I.;
L Submitted (Appr.1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; API65154; AAD45379.1; -.
R EMBL; API52376; AAD454941.1; -.
R EMBL; API55510; AAD54941.1; -.
R EMBL; BAF155510; AAD54941.1; -.
R EMBL; BAF14325; AAD41342.1; -.
R EMBL; API44325; AAD41342.1; -.
R EMBL; API44325; AAD41342.1; -.
R GO; GO:0004566; F:beta-djucuronidase activity; TAS.
GO; GO:0004566; F:proteoglycan metabolism; TAS.
R GO; GO:0004566; F:proteoglycan metabolism; TAS.
R GO; GO:0006029; P:proteoglycan metabolism; TAS.
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Pred. No. 1.9e-204;
1; Mismatches 0;
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Pappo O., Peretz T., Michal I.,
                                                PPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
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J., Myers R.M., Butterfield
D.E., Schnerch A., Schein J.
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Best Local Similarity 99.4
Matches 542; Conservative
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Q9UL39;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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Genew; HGNC.5164; HPSE.
InterPro; IPR005199; Glyco_hydro_79N.
Pfam; PF03662; Glyco_hydro_79n; 1.
Pfam; PF03662; Glyco_hydro_79n; 67B80ACD73C5A9A1_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Placenta;
MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.;
"Heparanase expression in invasive trophoblasts and acute vascu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycobiology 10:467-475 (2000).
EMBL; AF084467; AAD54516.1; -.
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                                                  LLRPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVTRNAK
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                                       LIRPIGPHGILSKSVQLNGLTIKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAK
                                                                                                                             FAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKV
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99.4%;
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Pred. No. 7.1e-
1; Mismatches
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Q9MYY0;
01-OCT-2000
01-JUN-2001
01-JUN-2002
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Mammalia; Eutheria;
Bovinae; Bos.
Q8KGKG
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EMBL; AF281160; AAP87301.2; -.
InterPro; IPRR005199; Glyco_hydro_79N.
Pfam; PP03662; Glyco_hydro_79n; I.
SEQUENCE 545 AA; 61076 MW; FAC4BD
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Kizaki K., Nakano H., Nakano H., Takahash
"Expression of heparanase mRNA in bovine
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Pred. No. 1.1e-1
35; Mismatches
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n bovine placenta during
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Q8K3K3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
enriched library, clone:A430101M04 product:heparanase, full insert
SEQUENCE FROM N.A.

STRAIN-(57BL/6J; TISSUB-Thymus;

STRAIN-(57BL/6J; TISSUB-Thymus;

Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Caladachi J., Alzawa K., Akimura T., Hara A., Hashizume W.,

Fukuda S., Furuno M., Hanagaki T., Haraka T., Hirozan

Hayashida K., Hayateu N., Hiramoto K., Hiracka T., Hirozan

Hayashida K., Hayateu N., Hiramoto K., Hiracka T., Kasuka

Hori F., Imotani K., Ishii Y., Kondo S., Konno H., Kouda W., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda W., Katch H., Kawai J., Kojima Y., Miyazaki A., Murata M., Nakamu
                                                                                                                                                                           STRAIN-C57BL/6J; TISSUE=Thymus;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Kegami T., Kashiwagi K.,

Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshika M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Thymus;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H., Plata A., Zhou Q., Ludwig D., Bohlen P., Kussie P.; "Cloning, expression, and purification of mouse heparanase."; Protein Expr. Purif. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
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STRAIN=C57BL/6J; TISSUE=Thymus;
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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"High-efficiency full-length cDNA
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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Mammalia; Eutheria;
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Sciurognathi; Muridae;
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Kouda M., Ko
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DE Heparanase.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; (R.
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RMBL; AY077467; AAL76083.1; -.
R EMBL; AX040471; BAC30600.1; -.
R EMBL; AR359507, AAQ15188.1; -.
R EMBL; AR359507; AAQ15188.1; -.
R MGD; MGI:1343124; Hpse.
R GO; GO:0005578; C:extracellular matrix (sensu Me
R GO; GO:0005578; C:extracellular matrix (sensu Me
InterPro; IPR005199; Glyco_hydro_79N.
INTERP03662; Glyco_hydro_79n; I.
SEQUENCE 535 AA; 60065 MW; 6E73A8302FB8A0DF
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=SJL/J; TISSUE=Spleen;
""and J., Hornby J
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07; Conservative
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     Chordata;
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51; Mismatches
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    Craniata; Ver
Sciurognathi;
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Heparanase.
Name=Hspe;
Rattus norvegicus (
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10116;
[1]
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ da
EMBL; AY151051; AAN41636.1; -.
GO; GO:0005578; C:extracellular matrix (sensu Me
InterPro; IPR005199; Glyco hydro 79N.
Pfam; PF03662; Glyco hydro 79n; 1.
SEQUENCE 535 AA; 59992 MW; 3748AEB3795C718A
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Li J.-P.,
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SEQUENCE FROM N.A.
MEDLINE=22841152; PubMed=12837765; DOI=10.1074/jbc.M300925200;
Gong F., Jemth P., Galvis M.L.E., Vlodavsky I., Horner A., Lin
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278:35152-35158(2003).
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Submitted (MAR-2001) to the EMBL/GenE EMBL; AF359508; AAQ15189.1; -...
InterPro; IPR005199; Glyco hydro 79N; I.
SEQUENCE 536 AA; 60479 MW; C434EC
  SEQUENCE FROM N.A. Podyma K.A., Yokote Submitted (SEP-1999)
                                                                                      MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200; Podyma-Inoue K.A., Yokote H., Sakaguchi K., Ikuta M., Yanagishita Podyma-rization of heparannase from a rat parathyroid cell line. J. Biol. Chem. 277:32459-32465(2002).
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Best Local
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Heparanase.
Gallus gallus (Chicken).
Gukaryota; Metazoa; Chordata; C
Eukaryota; Metazoa; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          090YK5;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                               MEDLINE-2136959; PubMed-11387326; DOI=10.1074/jbc.M102462200; MEDLINE-2136959; PubMed-11387326; DOI=10.1074/jbc.M102462200; Goldsbmidt O., Zcharia E., Aingorn H., Guatta-Rangini Z., Atzmu Michal I., Pecker I., Mitrani E., Vlodavsky I.; "Expression pattern and secretion of human and chicken heparanidetermined by their signal peptide sequence."; J. Biol. Chem. 276:29178-29187(2001).

EMBL; AY037007; AAK82648.1; -. Pfam; PF03662; Glyco hydro 79n; 1.

SEQUENCE 523 AA; 58386 MW; BEBOB7B18C9BF881 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF184967; AAF04563.1; -.
InterPro; IFR005199; Glyco hydro
Pfam; PF03662; Glyco hydro 79n; I
SEQUENCE 536 AA; 60568 MW; 62
                                                                                                                                                                                                                                                                    SEQUENCE
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Neognathae; Galliformes; Phasianidae; Phasiani
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75.7%;
    57.9%;
60.2%;
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21,
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Pred. No. 9.5e
51; Mismatches
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    Score
Pred.
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No. 6
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         6.8e-115;
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Length

heparanase

are

Atzmon

Phasianinae;

536

488

421 428 361 368

Matches

195

158

77

255 218

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RESULT QPHB3T/T QPHB3
                   Query Match
Best Local Similarity
Matches 250; Conser
                                                                                            SEQUENCE FROM N.A.

McKenzie E.A., Tyson K., Stamps A.;

McKenzie E.A., Tyson K., Stamps A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ dail

EMBL; AF282887; AAC32323.1;

GO; GO:0005622; C:intracellular; TAS.

GO; GO:0030305; F:heparanase activity; TAS.

InterPro; IFR0055199; Glyco-hydro-79N.

Pfam; PF03662; Glyco-hydro-79n; 1

SEQUENCE 592 AA; 66580 MW; 95C384AD9A74258E
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R., Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., Page "Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member.";
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01-MAR-2001
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heparanase-like protein HPA2c.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9НВ37
Q9НВ37;
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                                     40.6%;
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16, Last sequence update)
24, Last annotation update)
         82;
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Pred.
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                                                                                                 95C384AD9A74258E
         Mismatches
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                                     No. 6.3e
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         189;
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       Indels
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; Homo.
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                                                                                                      RESULT

ORWING

DOWNO

OCCUPAN

      Query Match
Best Local Sim
Matches 249;
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                                                                                    Pessegue Satontas B.J.O.P.S.;

Submitted (SEP-2000) to the EMBL/C
EMBL; AJ299719; CAC82491.1; -.

Genew; HGNC:18374; HPSE2.

Pfam; PF03662; Glyco hydro 79n; 1.

SEQUENCE 592 AA; 66520 MW; 94°
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Q8WWQ2;
01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                               TISSUE=Prostate;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      TISSUE=Prostate,
Legoux P., Legou
                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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       Similarity 43.4
49; Conservative
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Primates;
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448

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40.3%; Score 1146.5; DB 2;
43.4%; Pred. No. 2.5e-77;
cive 82; Mismatches 190;
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the EMBL/GenBank/DDBJ
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Last sequence Last anno
                                                                                                   EMBL/GenBank/DDBJ
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annotation update)
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COC Homo
OC Eukar
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OX NCB1 | 7
RN [1] -
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RC TISSU
RA Legov
RL Legov
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Q8WWQ1;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                   Heparanase 3.
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                    Pessegue Safontas B.J.O.P.S.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL; AJ299720; CAC82492.1; -
Pfam; PF03662; Glyco hydro 79n; 1.
SEQUENCE 548 AA; 61771 MW; B8986303FC73A60
                                                                                                                                                                                                                                                                                                 Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                        35.7%;
                                                                                                                                                                                                                                                                                                 , O'Brien D., Salome M.;
to the EMBL/GenBank/DDBJ
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                                                       79;
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Last sequence update)
Last annotation updat
                                                                            Score 1015.5;
Pred. No. 1.66
                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                        B8986303FC73A60A CRC64;
                                                            Mismatches
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                                                                        5; DB 2;
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                                                            180;
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                    -PRPA-----QAQDVVDLDF
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                                                                                               Length
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                                                         Gaps
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ID Q9HB3
AC Q9HB3
DT 01-W3
DT 01-
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                                                                                                                   Query Match
Best Local S
Matches 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HB38;
Q9HB38;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Heparanase-like protein HPA2b.
Homo sapiens (Human)
                                                                                                                                                                                                SEQUENCE FROM N.A.

McKenzie E.A., Tyson K., Stamps A.;

McKenzie E.A., Tyson K., Stamps A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF282886; AAG23422.1; -.

InterPro; IPR005199; Glyco.hydro 79N.

Pfam; PF03862; Glyco.hydro.79n; I.

SEQUENCE 534 AA; 60063 MW; C3DE5E900CB338C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                       MEDIINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586; MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R. Hircock M., Patel S., Barry E., Stubberfield C., Terrett J., P. "Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member."; hepachem. Biophys. Res. Commun. 276:1170-1177(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHLVLLKEOFSNTYSNLILTARSLDKLYNSADCSGLHLIFALNALRRNPNNSWNSSSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQL-LLREHYQKKFKNSTYSRSSVDVLYTFANCSGLDLIFGLNALLRTADLQWNSSNAQL
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  FLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIF----DPKKEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLMASVQGSKRR------KLRVYLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLDYCSSKGYNISWELGNEPNSFLKKADIFINGSQLGEDYIQLHKLLRK-STFKNAKLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F----DPKKESTFEERSYWQSQVNQDI------
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                                       PPACLAPGALYLALLLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN
                                                                              PLGPLSPGAL-----
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                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                      33.0%;
                                                                                                             78;
                                                                                                                 Score 936.5; DB 2;
Pred. No. 1.3e-61;
8; Mismatches 168;
                                                                            -----PRPA-----QAQDVVDLDFFTQEPLHLVSPS
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                                                                                                                   Indels 111;
                                                                                                                                                         Length
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                                                                                                                      Gaps
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Query Match
Best Local S
Matches 202
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Q9HB39;
O1-MAR-2001 (TIEMBLICEL 1
01-MAR-2001 (TIEMBLICEL 1
01-MAR-2004 (TIEMBLICEL 1
01-MAR-2004 (TIEMBLICEL 1
                                                                                                                                                                  SEQUENCE FROM N.A.

McKenzie E.A., Tyson K., Stamps A.;

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AF282885; AAG23421.1; -.

PIR; JC7506; JC7506.

InterPro; IPR005199; Glyco_hydro_79N.

Pfam; PF03662; Glyco_hydro_79n; I.

SEQUENCE 480 AA; 53900 MW; F75F89F67AC1FF83 CRC64;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDINE=20483645; PubMed=11027606; DOI=10.1006/bbrc.2000.3586;
MCKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.

"Hirook M., Patel S., Barry E., Stubberfield C., Terrett J., P.

"Cloning and expression profiling of Hpa2, a novel mammalian heparanase family member.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Heparanase-like protein HPAZa.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                          Similarity
                  PPACLAPGALYLALLLHLSLSSQAGDRRPLPVDRAAGLKEKTLILLDVSTKNPVRTVNEN
                                                               PLGPLSPGAL-----
                                                                                                                                                                                                                                                                                                                                                      Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLTLYAINLHNVTKYLRLPYPFSNKQVDKYLLRPLGPHGLLSKSVQLNGLTLKMVDDQTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDPLPDYWLSILEKKIVGTKVIMASVQGSKRR-----KIRVYLHCTNTDNPRYKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIWLEGVVTTSAGGTNNLSDSYAAGFLWLNTLGMLANQGIDVVIRHSFFDHGYNHLVDQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVWLGETSSAYGGGAPLLSDTFAAGFMWLDKLGLSARMGIEVVWRQVFFGAGNYHLVDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLDGFMKVAGSTVDAVTWQHCYIDGRVVKVMDFLKTRLLDTLSDQIRKIQKVVNTYTPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLKSFLKAGGEVIDSVTWHHYYLNGRTATREDFLNPDVLDIFISSVOKVFQVVESTRPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TÉPNNYRTMHGRAVNGSQLGKDÝTQLKSLLQPIRTYSRÁSLYGÞNIGRÞRKNVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  Res. Commun. 276:1170-1177(2000).
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                                                                                                                                    Length 480;
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                                                                                                                                              deJong P.J., Shimada T.;

"Genomic sequence of a 320-kb segment of the mori containing a kettin ortholog.";

Mol. Genomics 269:137-149(2003).

EMBL; AB079860; BAB85191.1;

EMBL; AB090307; BACL0612.1;

InterPro; IPR005199; Glyco hydro 79N.

Pfam; PP03662; Glyco hydro 79n; T.

SEQUENCE 515 AA; 59769 MW; PB8100AB86EI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8T108;
Q8T108;
01-JUN-2002
01-JUN-2002
05-JUL-2004
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=p50, TISSUE=Posterior silkgland;
Koike Y., Mita K., Suzuki M.G., Maeda S.,
                                                                                                                                                                                                                                                                                                                                                                                                           Heparanase-like protein.

Name-Emhepa;
Bombyx mori (Silk moth).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptrora; Bendopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.

NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                          Match
                                                                                     183;
            42
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                                                                                                     Similarity
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QEDIKLISEDFLSFGID-TIEIENYNRINYSDTRLRELAAALSPARLRLGGTMSERLIF-
                                QEPLHLVSPSFLSVTIDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVIPPVTMGFFVVKNVNALAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYLRLPYPFSNKQ', L'I', L'EPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKLVGTKVLMASVQGSKRR------KLRVYLHCTNTDNPRYKEGDLTLYAINLHNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVTWQHCYIDGRVVKVMDFLKTRLLDTLSDQIRKIQKVVNTYTPGKKIWLEGVVTTSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GINNLSDSYAAGELWINTLGMIANQGIDVVIRHSFEDHGYNHLVDQNFNPLPDYWLSLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPLLSDTFAAGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDDPLPDYWLSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSVTWHHYYLNGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGG
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(TrEMBLrel.
                                                                                   Conservative
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21,
27,
                                                                                 83;
                                                                               Score 696; DB 2;
Pred. No. 1.4e-43;
3; Mismatches 182
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Last annotation update)
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456 521 396 461

410 336

276 350 216 290 156 148 171

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                                                                                                                                  Query Ma
Best Loc
Matches
                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ date EMBL; All33421; CAB62595.1; -.
PIR; T45608; T45608.
InterPro; IPR005199; Glyco hydro 79N.
InterPro; IPR001254; Peptidase_SI.
Pfam; PF03662; Glyco hydro 79n; 1.
PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 521 AA; 57831 MM; 07D8664A4B305CC2 (
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O9SDA1;
O1-MAY-2000 (TrEMBLrel. 13, Createu,
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update,
O1-MAY-2000 (TrEMBLrel. 26, Last annotation update)
O1-MAR-2004 (TrEMBLrel. 13, Createu,
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update,
O1-MAY-2000 (TrEMBLrel. 26, Last sequence update,
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM Bevan M., Van Volckaert G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotytedons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                           Match
Local Similarity
168 154; Conserv
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                                                        LGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQSQVNQDICKYGSIPP
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521 AA
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Van Der Schueren J., Chuang Y.J., Voet M., Rob
G., Bancroft I., Mewes H.W., Lemcke K., Mayer
(DEC-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                  Conservative
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                                                                                                                                                                 Score 416; DB 2;
Pred. No. 1.6e-22;
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NGKSLKPTATGDIPSL-EPVLRSVNSPLNVLPLSMSFIVLPNFDASAC
                         NGLTLKWVDDQTLPPLMEKPLRP-GSSLGLPAFSYSFFVIRNAKVAAC
                                                     VSNGINVVLNAESRKKKSLLDTLKRPFSWIGSKASDGYLNREEYHLTPENGVLRSKTMVL
                                                                                                          ALLWHRLMGKGVLAVQTDGPP--QLRVYAHCSK-----GRAGVTLLLINLSNQSDFTVS
                                                                                                                                                                YNSGGRHVSDTFIDSFWYLDQLGMSARHNTKVYCRQTLVG-GFYGLLEKGTFVPNPDYYS
                                                                                                                                                                                THHIYNLGSGNDPALVKKIMDPS----YLSOVSKTFKDVNOTIQEHGPWASPWVGESGGA
                                                                                                                                                                                                                                               TWHHYYLNGRT---ATREDFLNPDVLDIFISSVQKVF----QVVESTRPGKKVWLGETSSA
                                                                                                                                                                                                                                                                                                       GSQLGEDYIQLHKLLRKSTFKNAKLYGPDVGQP----RRKTAKMLKSFLKAGGEVIDSV
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                                                                             ----RLPYPFS---NKQVDKYLLRP---LGPHG--LLSKSVQL
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Search completed: February 28, 2005, 06:08:39
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 A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp2990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003as:*
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2842
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1220.994 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Regult No.	Score	Query Match L	Length	BB	ID	Description
1	2842	100.0	543	N	AAY02345	Aay02345 A human h
N	2842		543	w	5759	Human he
ω	2842		543	w	AAB08849	
4	2842	8	543	ω	AAY52990	Human
u	2842	100.0	543	4.	AAY97635	Human
0	2842	•	543	ű	ABB07813	Human he
7	2842	•	543	7	ADG88800	Human
8	2842	•	543	8	ADL16379	
9	2842	100.0	543	8	ADM48716	Human
10	2842	•	592	N	AAY02346	A huma
11	2842	•	592	ω	AAB08850	Aab08850 Amino aci
12	2842	100.0	592	7	ADG88804	Human
13	2842	٠	592	8	ADL16383	Adl16383 Human hep
14	2842	•	592	8	ADM48720	Human
15	2838	٠	543	N	AAY17082	Aay17082 Human hep
16	2838	•	543	4	AAB86206	Human
17	2838	99.9	543	7	ADD18950	Add18950 Human dis
18	2838	٠	543	8	ADK52086	
19	2838	•	543	œ	ADM48759	
20	2838	•	543	œ	ADN05074	Adn05074 Antipsori
21	2838	٠	543	ထ	ADN04902	Adn04902 Antipsori
22	2838	٠	543	œ	ADQ80372	Adq80372 Heparanas
23	2838	•	543	8	ADR88210	
24	2838	99.9	543	8	ADP25079	
25	2838	٠	588	N	AAY30124	A hi

The specification describes a polypeptide having heparanase (hp) activity. The recombinant protein is used as a modulator of heparinbinding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disintegration of neurodegenerative plaques. Heparanase may be useful for

Claim 6; Fig 1; 63pp; English. New human polynucleotide useful and inflammation. N-PSDB; AAX35648.

for treating angiogenesis, restenosis,

WPI; 1999-302255/25.

Pecker I, Vlodavsky

Feinstein

4	44	3	42	41	40	39	38	37	36	3 5	34	33	32	31	30	29	28	27	26
2146	2146	2146	2146	2661.5	2667.5	2667.5	2673.5	2673.5	2737	2764	2817	2817	2817	2826	2826	2832	2832	2832	2832
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ALIGNMENTS

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RESULT 1
AAY02345
Heparanase; hp; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersclerosis; inflammation; neurodegenerative disease; neutralise
                                                                                                                                                                                                                                                                                                                                         plasma heparin; micrometastasis; autoimmune lesion; renal failure.
                                                                                                                                                                                 (INSI-) INSIGHT STRATEGY & MARKETING LTD. (HADA-) HADASIT MEDICAL RES SERVICES & DEV. (FRIE/) FRIEDMAN M M.
                                                                                                                                                                                                                          02-SEP-1997;
02-JUL-1998;
                                                                                                                                                                                                                                                          31-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                       A human heparanase protein.
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98US-00109386.
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Matches 543
              Human; heparanase; hpa; genetic modification; expression; anticancer; angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumon anti-atherosclerotic; anti-inflammatory; antineurodegeneration; heparan sulphate; heparin-binding growth factor; tumour angiogenesis; metastasis; wound healing; restenosis; atherosclerosis; inflammation; neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis micrometastasis; autoimmune lesion; kidney failure.
                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions such as wound healing, angiogenesis, restenosis, atherselerosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparanase can be used to neutralize plasma heparin, and anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimmune lesions, au renal failure in biopsy specimens, plasma samples, and body fluids. The present sequence represents human heparanase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The present invention describes genetically modified cells (A) containing CC a polynucleotide (I) that encodes a polypeptide with heparanase activity, CC and express recombinant heparanase (II). Heparanase cleaves heparan CC sulphate (HS) at specific intrachain sites, resulting in release of CC heparin-binding growth factors, enzymes and proteins that are sequestered by HS in basement membranes, extracellular matrix or cell surfaces. It CC may also be implicated in tumour anglogenesis and metastases. (II) is CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral CC potentially useful in wound healing and for treating angiogenesis (C restenosis, atherosclerosis, inflammation, neurodegeneration, viral CC infection and cystic fibrosis. It can also be used to neutralise heparin CC (an alternative to protamine) and to screen for specific inhibitors (potentially useful for treating cancer and metastases). Antibodies CC raised against (II) are used for immunodetection and diagnosis of CC micrometastases, autoimmune lesions and kidney failure. (A) provide (C activated/neutralised by a dedicated protease. The present sequence (C represents shuman hearanase)
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Matches 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Engineered cells that express recombinant heparanase, therapeutically, e.g. for treating angiogenesis and t specific inhibitors, potential anticancer agents.
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The present sequence represents a human protein with heparanase catalytic activity. The heparanase (hap) polynucleotide is useful in gene therapy, particularly in treating tumour, inflammation or autoimmunity.

Particularly, the polynucleotide is useful in modulating the bloavaliability of heparin-binding growth factors, cellular responses to heparin-binding growth factors, cellular responses to interleukin (II)-8), cell interaction with plasma lipoproteins, cellular susceptibility to certain viral and some bacterial and protozoa infections, or disintegration of neurodegenerative plaques. The polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral, bacterial or protozoa infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; heparanase; gene therapy; tumour; inflammation; autoimmunity; heparin-binding growth factor; cytokine; neurodegenerative plaque; wound healing; infection; burn; angiogenesis; tetenosis; atherosclerosis; inflammation; neurodegenerative disease; Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
                                                                                                                                                                                                                     Claim
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                                                                                                           Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic; antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic; metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma; mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes; inflammation; haemorrhagic nephritis; nephrotic syndrome; autoimmune disease; anticancer; kidney disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 543
                                                                                                                                                                                                  Human heparanase protein sequence
                                                                                                                                                                                                                                                                           AAY52990
                                      11-NOV-1999.
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29-APR-1999;

99WO-US009255

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Query Match
Best Local S
Matches 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 543
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                              RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
                                                                                      ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL
                                                                                                                    ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPFSNKQVDKYLL
                                                                                                                                                                                                               AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDPLPDYWLSLLFKKLVGTKVLM
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Pred. No. 2.5e-273;
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                                                                                                                                                                                                                                                                                                                                      This sequence represents a heparanase of the invention. The heparanase DNA and protein sequences are useful in wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, pulmonary diseases, neurodegenerative diseases (such as Scrape, Alzheimer's disease, and Creutzfeldt-Jakob disease) or viral infections. The heparanase coding
                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides and polypeptides that are distantly homologous heparanase, useful in wound healing, as well as in gene therapy profor angiogenesis, restenosis, atherosclerosis, or inflammation.
                                                                                                                                                                                                                                                                                                       Sequence 543 AA;
                                                                                                                                                                                                                                                                                                                               sequence is particularly useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 64-65; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-137930/14.
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                                                         GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEDNSFLKKADIFINGS
                                                                                                          QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
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                                          GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS
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Pred. No. 2.5e-273;
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The invention relates to an isolated avian and reptile nucleic acid, encoding a polypeptide with heparanase catalytic activity. The signal peptide of the nucleic acid can be used to express membrane-associated c secreted proteins in heterologous expression systems. The encoded polypeptides can be used to prevent tumour angiogenesis, metastasis and invasion, and to intervene with pathologies associated with impaired heparin-binding growth factors, cellular responses to heparin-binding growth factors, cellular responses to heparin-binding mouth factors, cellular responses to heparin-binding seconds.
                                                                                                                                                                                                                Nucleic acid encoding avian and reptile heparanase polypeptide is to treat various heparin-related disorders and the signal peptide useful in production of membrane-targeted or secreted recombinant
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                                                                                                                                                               Disclosure; Fig la; 39pp; English.
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Query Match
Best Local Similarity
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                                                                                         Wound healing; heparanase; ulcer; burn; laceration; surgical incision; necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy
                                                                                                                                                          Human hpa protein.
US2003161823-A1
                                                                                                                                                                                                                                                                                                    ADG88800 standard;
                                                                                      necrosis; pressure
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Pred. No. 2.5e-273;
Mismatches 0;
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Best Local S
Matches 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to methods and compositions for inducir and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incisic necrosis, pressure wound, diabetic ulcer and to induce or accelerate angiogenesis. The present sequence is human hpa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1999;
06-FEB-2001;
05-SEP-2001;
19-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition for treating a wound comprising recombinant useful to induce or accelerate wound healing and induce
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DB; ADG88799, AL
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                            RPLGPHGLLSKSVQLNGLTLKNVDDQTLPPLMEKPLRPGSSLGLPAFSYSFFVIRNAKVA
                                           RPLGPHGLLSKSVQLNGLTLKMVDDQTLPPLMEKPLRPGSSLGLPAFSVSFFVIRNAKVA
                                                                             ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPPSNKQVDKYLL
                                                                                               ASVQGSKRRKLRVYLHCTNTDNPRYKEGDLTLYAINLHNVTKYLRLPYPESNKQVDKYLL
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) VLODAVSKY I.
) YACOBY-ZEEVI O.
) PECKER I.
) FEINSTEIN E.
                                                                                                                                                AGFMWLDKLGLSARMGIEVVMRQVFFGAGNYHLVDENFDDLPDYWLSLLFKKLVGTKVLM
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New antisense oligonucleotide hybridizable with a polynucleotide encoding a polypeptide with heparanase activity, useful for treating diseases such polypeptide cancer and autoimmune disorders.

Claim 3; SEQ ID NO 10; 108pp; English

CC polymicleotide or a polymicleotide analogue of at least 10 bases being catalytic activity. Also included are amethod of in vivo downregulating contracterised by heparanase activity, comprising administering the ASO in vivo), a method contracterised by heparanase activity, comprising administering the ASO in vivo), a method contracterised by heparanase activity, composition comprising administering the ASO and a carrier, an antisense nucleic acid construct (comprising a promoter contribution contribution) and a polymicleotide sequence directing the ASO and a contisense RNA sequence of at least 10 bases being hybridisable in vivo antisense nucleic acid construct (comprising a promoter contribution contribution) and comprising the ASO and a contisense contribution activity, and the synthesis of an contribution of a comprising heparanase activity (comprising doministering in vivo antisense oligonicleotide construct), a pharmaceutical composition comprising the antisense mucleic acid construct), a pharmaceutical composition contisense oligonicleotide comprising a polymicleotide or a polymicleotide strand encoding a polymicleotide strand being contribution and conditions, with a portion of a polymicleotide strand being contribution are useful for the prevention and/or treatment of the prevention are useful for the prevention and/or treatment of as heparanase catalytic activity. The methods and compositions of the construct of the prevention and contributy, such as heparanase dependent cancer, cancer, autoimmune reaction and contributy. Such construct is a human heparanase is located on chromosome 4. The invention relates to an antisense oligonucleotide (ASO) polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide (ASO) polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide (ASO) polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide or a polynucleotide analogue of at least 10 polynucleotide analogue of

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VLODAVSKY I
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic non-human animal expressing heparinase, useful as models for human disease, such as cancers, viral infection, neurodegenerative diseases, restenosis, atherosclerosis and pulmonary disorders.
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Chajek-Shaul
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(CHAJ/)
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GOLDSHMIDT O.
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Pred. No. 2.5e-273;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                            The specification describes a polypeptide having heparanase (hpa) activity. The recombinant protein is used as a modulator of heparin-binding growth factors, cellular responses to heparin-binding growth factors and cytokines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or conditions such as wound healing, angiogenesis, restenosis, atheracterosis, inflammation, neurodegenerative diseases, and viral heparin, and anti-heparanase can be used to neutralize plasma immunodetection and diagnosis of micrometastases, autoimune lesions, an present sequence represents human heparanase
                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6;
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(FRIE/)
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02-JUL-1998;
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                                                                                                                                                                                                                                                                        592 AA;
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tive 0; Mismatches 0;
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New polynucleotides encoding a polypeptide having heparanase activity, useful in wound healing and in gene therapy, particularly in treating tumor, inflammation, autoimmunity, neurodegenerative diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heparanase; gene therapy; tumour; inflammation; autoheparin-binding growth factor; cytokine; neurodegenerative wound healing; infection; burn; angiogenesis; restenosis; atherosclerosis; inflammation; neurodegenerative disease;
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CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy, CC particularly in treating tumour, inflammation or autoimmunity. CC particularly, the polynucleotide is useful in modulating the CC bioavailability of heparin-binding growth factors, cellular responses to CC interleukin (II)-8), cell interaction with plasma lipoproteins, cellular CC susceptibility to certain viral and some bacterial and protozoa and interactions, or disintegration of neurodegenerative plaques. The CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burne), and in the treatment of angiogenesis, restenosis, catherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral, (X
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01-MAR-1999;
06-FEB-2001;
05-SEP-2001;
19-NOV-2001;
                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods and compositions for inducir and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incisis necrosis, pressure wound, diabetic ulcer and to induce or accelerate angiogenesis. The present sequence is human SK-hepl protein.
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(VLOD/)
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YACOBY-ZEEVI
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            NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA
                                                                                                   GLDL1FGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNEFNSFLKKADIFINGS
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NGRTATREDFLNPDVLDIFISSVQKVFQVVESTRPGKKVWLGETSSAYGGGAPLLSDTFA
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## 99US-00258892.
## 2001US-00776874.
## 2001WO-IL000830.
## 2001US-00988113.
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Pred. No. 2.9e-273;
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RESULT 13
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The invention relates to an antisense oligonucleotide (ASO) comprising a C polynucleotide or a polynucleotide analogue of at least 10 bases being c polynucleotide strand encoding a polypeptide having heparanase c activity. Also included are a method of in vivo downregulating c attalytic activity. Also included are a method of in vivo downregulating of treating a subject suffering from a pathological condition of c characterised by heparanase activity, comprising administering the ASO in vivo), a method c characterised by heparanase activity, comprising administering ASO to c carrier, an antisense nucleic acid construct (comprising heparanase c c c sequence and a polynucleotide sequence directing the ASO and a c sequence and a polynucleotide sequence directing the synthesis of an c sequence and a polynucleotide sequence directing the synthesis of an c under physiological conditions, with a polynucleotide strand encoding a compresulating heparanase activity (comprising administering in vivo c antisense nucleic acid construct), a method of in vivo antisense nucleic acid construct and a carrier, and an comprising the antisense nucleic acid construct and a carrier, and an antisense oligonucleotide comprising a polynucleotide or a polynucleotide
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08-NOV-1999;
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RESULT 14
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ID ADM48
XX ADM48
AC ADM48
XX O3-JU
XX O3-JU
XX Human
XX Trans
KW neurc
KW human
XX homo ADM48720 standard; protein;

592

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03-JUN-2004 (first entry)

Human SK-hep1 hpa protein.

Transgenic animal; heparanase; cancer; viral infection; restenosis; neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa

Homo sapiens

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase are operably linked in the exogenous polynucleotide such that human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, to be used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atherosclerosis and pulmonary disorders. The present sequence is human SK-hepl hpa protein used in the
                                                                                                                                                                                                                                                                                                                                                         Sequence 592
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19-NOV-2001;
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PECKER I.
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GOLDSHMIDT O.
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                                                                                                             GLDLIFGLNALLRTADLQWNSSNAQLLLDYCSSKGYNISWELGNERNSFLKKADIFINGS
                                                                                                                                           QVNQDICKYGSIPPDVEEKLRLEWPYQEQLLLREHYQKKFKNSTYSRSSVDVLYTFANCS
                                                                                                                                                                                                              IDANLATDPRFLILLGSPKLRTLARGLSPAYLRFGGTKTDFLIFDPKKESTFEERSYWQS
                                         QLGEDYIQLHKLLRKSTFKNAKLYGPDVGQPRRKTAKMLKSFLKAGGEVIDSVTWHHYYL
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RESULT 15
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                                                                                    The invention relates to nucleic acid sequences that encode heparanase enzymes having endoglucuronidase activity. Recombinant heparanases are capable of removing the HS side chain from heparan sulfate proteoglycan (HSPG). Sulfated oligosaccharides, sulphonates or HSPG can be used to inhibit heparanase, this is useful for treatment of a physiological or medical condition associated with elevated heparanase activity, such as metastasis, angiogenesis, wound healing, angioplasty-induced restenosis, arteriosclerosis, atherosclerosis and inflammation. The human, murine and rat heparanases can be used to enhance wound healing, especially associated with tissue development and repair. The conditions mentioned above can be diagnosed using specific antibodies, and also using primers and probes specific for the heparanase polymucleotides. Other uses of the heparanases include sequencing sulfated molecules such as HSPG. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides encoding mammalian endoglucuronidases, heparanases, useful to promote wound healing.
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Sequence

sequence

represents a human heparanase

Search c	DЪ	Ş	Db	9	₽ \$	P Db	δ	Db	o 8	₹ 5	} ₽	γQ	В	γ	DЬ	γ	đđ	γQ	Query M Best Lo Matches
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Pecker, I., Vlodaveky, I. and Feinstein, E.

Polynucleotide encoding a polypeptide havir

and expression of same in transduced cells

Patent: US 5968822-A 9 19-OCT-1999;

Location/Qualifiers
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                                                                                                                 CTAGAGCTTTCGACTCTCCGCTGCGCGGCAGCTGGCGGGGGGAGCAGCCAGGTGAGCCCA
CCATTGACGCCAACCTGGCCACGGACCCGCGGTTCCTCATCCTCGTGGGTTCTCCAAAGC
                          ACCTGGACTTCACCCAGGAGCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA
                                                      CGCTGGGTCCCCTTGCCCCTGGCGCCCCGACCTGCGCAAGCACAGGACGTCGTGG
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from patent US 5968822.
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tive 0; Mismatches
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241 CCATTGACGCCAACCTGGCCACGG	1321 TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACA 1380	. 5
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61 AGATGCTGC 121 CGCTGGGTC 	.141	, 음 성
Db 1 CTAGAGCTTTCGACTCTCCGCTGC Qy 61 AGATGCTGCTGCGCTCGAAGCCTG		, p. 64
Matches 1721; Conservative 0; Free Conservative Conservation 0; Free Con	1021 TITCATCTGTGCAAAAGTTTTTCCAGGTGGTTGAGAGCACCAGGCCTGGCAAGAAGGTCT 1080 	B 8
itch 100.0%;	961 TGAATGGACGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTA 1020 	р Q
FEATURES Location/Qualific Source 11721 /organism="unknov/mol/type="un	901 AGASCTTCCTGAAGGCTGGTGGAGAAGTGATTGATTCAGTTACATGGCATCACTACTATT 960 	₽ 5
S Pecker, I., Vloo Polynucleotide and expression L Patent: US 5968	מי — על	, p 44
SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1721)	781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840 	β .Q
DEFINITION Sequence 11 from patent U ACCESSION AR080680 VERSION AR080680.1 GI:10007410 KEYWORDS	721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780 	, B &
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CY 1681 CTGCTTGCATCTGAAATAAAA Db 1681 CTGCTTGCATCTGAAAATAAAA	00	5 8 8
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301 TTCGTACCTTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAG 360
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Mismatches
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a polypeptide having heparanase activity
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CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG
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                                                                   TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACA 1380
                                                                                                                                 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA 1320
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man,Y. and Perets,T. probes and their use in research and 2001;	Unknown. Unknown. Unklassified. 1 (bases 1 to 1721) 1 (bases 1 to 1721) 1 (pases 1 to 17245-A 1 23-JAN-2001 1 (pases 1721) 2 (pases	SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES BOUTC ORIGIN
DNA linear PAT 16-MAY-2001 5.	AR125603 1721 bp Sequence 1 from patent US 617754 AR125603 AR125603.1 GI:14111665	RESULT 3 AR125603 LOCUS DEFINITION ACCESSION VERSION VERSION
TCCTGACACTG 1721 TCCTGACACTG 1721	681 CTGCTTGCATCTGAAAATAAAATATACTAGTCCTGACACTG	Qy 1
GTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1 	621 GTTCACTGGGCTTGCCAGCTTTCTCATATA	Qy 1 Db 1
TAAAGATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1 	.561 TAAAGATGGTGGATGATCAAACCTTGCCAC	Qy 1 Db 1
TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560 	501 TAAGACCTTTGGGACCTCATGGATTACTTT	Qy 1 Db 1
TTTCTAACAAGCAAGTGGATAAATACCTTC 1 	1441 TCACCAAGTACTTGCGGTTACCCTATCCTTTTTCTAACAAGCAAG	Qy 1 Db 1
TAACTCTGTATGCCATAAACCTCCATAACG 1440	181 CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG	Db 13

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medical applications
Patent: US 6177545-A 3 23-JAN-2001;
Location/Qualifiers
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Db 241 CCATTGA	DY 1501 TARGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560	ર્
Qy 241 CCATTGA	Db 1441 TCACCAAGTACTTGCGGTTACCCTATCCTTTTTCTAACCAAGTGGATAAATACCTTC 1500	밁
Db 181 ACCTGGA	DY 1441 TCACCAAGTACTTGCGGTTACCCTATCCTTTTTCTAACAAGCAAG	Ş
Oy 181 ACCTGGA	Db 1381 CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 1440 1381 CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCCATAACG 1440	당 성
121	1321 TGGCAAGCGTGCAAGGTTCAAAGAGAAGCTTCGAGTATACCTTCATTGCACAAACA	문
Db 61 AGATGCTV		ð
Qy 61 AGATGCT	1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA 1320	밁
Db 1 CTAGAGC	DY 1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA 1320	Ş
1 CT2	1201 TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTACATTTAGTGGATGAAAACTTCGATC 126	망
Best Local Similarion Matches 1721: Consu	1201 TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACTTCGATC	§
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	1081	밁
source	29 1081 GGTTAGGAGAAACAAGCTCTGCATATGGAGGCGGGAGCGCCCTTGCTATCCGACACCTTTG 1140	ð
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C07K16/00	DY 1021 TTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGAGGCCCAGGCCTGGCAAGAAGGTCT 1080	ð
	39 961 TGAATGGACGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTA 1020	무 5
E	901 AGAGCTTCCTGAAGGCTGGTGGAGAAGTGATTGATTCAGTTACATGGCATCACTACTATT	?
JOURNAL Patent: JI	901	Ş
AUTHORS PECKET, 1. TITLE Heparanasumedical au	941 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAAGA	90
	2Y 841 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAAAAGACGGCTAAGATGCTGA 900	Ş
MS	DY 781 CGCAGTTAGGAGAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840	음 ઇ
ACCESSION BD193236. VERSION BD193236. KEYWORDS JP 200251	721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCATCAATGGGT 780	밁
Z	OY 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780	ð
	661 ACAGTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCTCCAAGGGGTATAACATTTCTT	문
RESULT 5	DY 661 ACAGTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTT 720	S
Db 1681 CTGCTTG	601 CAGGACTGGACTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGA	밁
Qy 1681 CTGCTTG	601 CAGGACTGGACTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGA	ð
Db 1621 Ġrrcacr	541 TCAAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT	뮍
Qy 1621 GTTCACTV	541 TCAAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTTGCAAACTGCT	ş
Db 1561 TAAAGAT	TACGGTTGGAATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGT	B 8
Qy 1561 TAAAGAT	421 CTCAAGTCAACCAGGATATTTTGCAAATATGGATCCATCC) g
Db 1501 TAAGACC		2

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100.0%; Score 1721;
city 100.0%; Pred. No. 0;
nervative 0; Mismatches
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I, Vlodavsky,I., Friedman,Y. and Perets,T.

Respecific molecular probes and their use in research and applications

JP 2002512533-A 1 23-APR-2002;

STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
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occus equi
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                       ACGCCAACCTGGCCACGGACCCGCGGTTCCTCATCCTCCTGGGTTCTCCAAAGC
                                                                   ACTICITCACCCAGGAGCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA 240
                                                                                                                                                                                                                  CTTTCGACTCTCCGCTGCGCGGCAGCTGGCGGGGGGAGCAGCCAGGTGAGCCCA
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MAY-1998 US 09/071739
S PECKER, IRARAEL VLODAVSKY, YAEL FRIEDMAN, TUVIA PERETS PC
0,C07K16/40,G01N33/53,C07H21/02,C7H21/04,A61K39/395 CC
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CGCCAACCTGGCCACGGACCCGCGGTTCCTCATCCTCCTGGGTTCTCCAAAGC
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/mol_type="genomic DNA"
/db_xref="taxon:1336"
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Db 61 Qy 121	1321 TGGCAAGCGTGCAAGGTTČAAAGAĞAĞĞAĞĞTTČCAĞTAĞAĞTĞĞTĞĞTĞĞTTĞCAĞAACA 1380 1381 CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCCATAAACCTCCATAACG 1440	Qy Lb
\$ &	TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACA	\$ 8
99 V2	1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA 1320 	₽ <i>\$</i>
Query Match Best Local S Matches 1721		d d
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COMMEN	961	\$ B &
JOURNAL		B :
REFERENCE AUTHORS TITLE	91 AGAGGTTCCTGAAGGTCCTGAAGGTCAAGGAAAAGACGGCTAAGATGCTGA 900 841 ATGCAAAACTCTATGGTCCTGATGTTCGTCAAGAAAGACGGCTAAGATGCTGA 900 841 ATGCAAAACTCTATGGTCCTGATGTTTGGTCAGCCTCGAAGAAGACGGCTAAGATGCTGA 900 901 AGAGGTTCCTGGAAGCTGCTGCAAGATGCTGA	
SOURCE ORGANISM	81	\$ B &
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RESULT 6 BD193237 LOCUS		B &
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Q B	481 TACGGTTGGAATGGCCCTACCAGGAGCAATTGCTGCTACTCCGAGAACACTACCAGAAAAAGT 540 541 TCAAGAACACTACTCTACTTCAAGAACACTACCAGAAAAAAGT 540	Q D
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CGCTGGGTCCCCTCTCCCCTGGCGCCCTGCCCCGACCTGCGCAAGCACAGACGTCGTGG 180
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(Cases 1 to 1721)

(Cases 1 to 1721)

(Caryin, Vlodavsky,I., Friedman,Y. and Perets,T.

recri., Vlodavsky,I., Friedman, Turia Perets, Israel, Israel
                                                                                                                                                                                                                                                  CTTTCGACTCTCCGCTGCGCGGCAGCTGGCGGGGGGGAGCAGGTGAGCCCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Streptococcus equi"
/mol_type="genomic DNA"
/db_xref="taxon:1336"
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1201 TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACTTCGATC 1260 	1141 CAGCTGGCTTTATGTGGCTGGATAAATTGGGCCTGTCAGCCCGAATGGGAATAGAAGTGG 1200 	1081 GGTTAGGAGAAACAAGCTCTGCATATGGAGGCGGAGGCGCCTTGCTATCCGACACCTTTG 1140	1021 TITCATCIGIGCAAAAAGITITCCAGGIGGITGAGAGACCCAGGCCIGGCAAGAAGGICI 1080	961 TGAATGGACGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTA 1020 	901 AGAGCTTCCTGAAGGCTGGTGGAGAAGTGATTGATTCAGTTACATGGCATCACTACTACT 960 	841 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAGACGGCTAAGATGCTGA 900 	781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840 	721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780 	661 ACAGITCIAATGCICAGTIGCICCIGGACTACTGCICTICCAAGGGGTATAACATITCIT 720	601 CAGGACTGGACTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGA 660	541 TCAAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAAACTGCT 600	481 TACGGTTGGAATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGT 540	421 CTCAAGTCAACCAGGATATTTGCAAATATGGATCCATCCCTGCTGATGTGGAGGAGAAGT 480 	361 ACTTCCTAATTTTCGATCCCAAGAAGGAAGCATCAACCTTTGAAGAGAAGATTACTGGCAAT 420 	301 TTCGTACCTTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAG 360	241 CCATTGACGCCAACCTGGCCACGGACCCGCGGTTCCTCATCCTCCTGGGTTCTCCAAAGC 300	181 ACCTGGACTTCTTCACCCAGGAGCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA 240
Key FT 80		CC St. 00, C121	PECKER, PECKER, OF GILBO	PD 144 PF 29 PR 01.	JOURNAL Patent: INSIGHT COMMENT OS Un.	AUTHORS Artzi, H Shlomi, Shlomi, TITLE Cells go	-	ACCESSION BD205231 VERSION BD205231 VERSION BD205231	RESULT 7 BD205238 LOCUS BD20523	Db 1681 CTGCT	1621	1561	1501		1381	1321	1261 1261 1321

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TGCATCTGAAAATAAATATACTAGTCCTGACACTG
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Topology: Linear;
Cells genetically modified for exp.
Cells genetically modified for exp.
Cells genetically modified for exp.
Apparamase and
method, and method of purifying reference
Location/Qualifiers
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''mider Bes 1 to 1721)
H.B., Hershkovitz,M.A., Zeevi,O.Y., Pecker,I., Peleg,Y.,
Y., Moskowitz,H., Miron,D., Gilboa,A. and Mimon,M.
genetically modified for expressing recombinant heparanase thod, and method of purifying recombinant heparanase thod, and method of purifying recombinant heparanase up 2002513560-A 1 14-MAY-2002;
T. STRATEGY AND MARKETING LTD /09,C07K16/40,C12N1/19,C12N1/21,C12N5/10,C12N9/24,C12N15/ 2N5/00 9-APR-1999 JF 2000547200 1-MAY-1998 US 09/071618,02-MAR-1999 US 09/260038 BEN ARTZI,MATY AYAL HERSHKOVITZ,ORON YACOBY ZEEVI,IRIS nidentified P 2002513560-A/1 2513560-A/1. tified 38 1721 bp DNA linear PAT 17-JUL-20 genetically modified for expressing recombinant heparanase thod, and method of purifying recombinant heparanase. ADELENE MIMON DAV PELEG, YINON SHLOMI, HAIM MOSKOWITZ, DEPHNA MIRON, AYELET sified. 8.1 GI:33015008 /organism='Unidentified'. for expressing recombinant recombinant heparanase. PAT 17-JUL-2003 გ PI Ŧ PC ΡI

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BD205239 LOCUS BD205239 BD205239 Cells genetically modified for expressing recombinant heparanase and method, and method of purifying recombinant heparanase. BD205239 VERSION BD205239 VERSION BD205239 BD205239 JP 2002513560-A/2. SOURCE ORGANISM unidentified unclassified. 1 (bases 1 to 1721) Attzi,H.B., Hershkovitz,M.A., Zeevi,O.Y., Pecker,I., Peleg,Y., TITLE Shlomi,Y., Moskowitz,H., Miron,D., Gilboa,A. and Mimon,M. Cells genetically modified for expressing recombinant heparanase and method, and method of purifying recombinant heparanase INSIGHT STRATEGY AND MARKETING LTD	OY 661 ACAGTTCTAATGCTCAGTTGCTCGACTACTGCTCTCCAAGGGGTATAACATTTCTT 720 Db 661 ACAGTTCTAATGCTCAGTTGCTCTGACTAGTGCTCTTCCAAGGGGTATAACATTTCTT 720 661 ACAGTTCTAATGCTCAGTTGCTCTGACTAGTGCTCTTCCAAGGGGTATAACATTTCTT 720 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780 Pb 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780 Pb 721 GGGAACTAGGCAAGAATTATATTCAATTGCATAAAACTTCTAAGAAGTTCAACTACTACTAAGAAGTCCACCTTCAAAA 840 Pb 781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTTCCACCTTCAAAA 840 Pb 781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840 Pb 781 CGCAGTTAGGAGAGAATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840 Pb 841 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAGAAGTCCACCTTCAAAA 840 Pb 841 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAGAAGAAGATGCTGA 900 PO	,
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Db 901 AGAGCTTCCTGAAGGCTGGTGGAGAAGTGATTCAGTTACATGGCATCACTACTATT 960 Qy 961 TGAATGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTTGGACATTTTTA 1020	FEATURES Location/Qualifiers 11721 /organism="unidentified" /mol_type="genomic DNA" /db_xref="taxon:32644"	Q F

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Ayal-Hershkovitz,M., Moskowitz,H., Miron,D., Gilboa,A., Mimon,M., Ben-Artzi,H., Yacoby-Zeevi,O., Pecker,I., Peleg,Y. and Schlomi,Y. Genetically modified cells and methods for expressing recombinant heparanase and methods of purifying same Patent: US 6348344-A 1 19-FEB-2002;
  ACAGTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTT
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661 ACAGTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTT 720	601 CAGGACTGGACTTGATCTTTGGCCTAAATGCGTTATTAAGAACAGCAGATTTGCAGTGGA 660	541 TCAAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT 600	481 TACGGTTGGAATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGT 540	421 CTCAAGTCAACCAGGATATTTGCAAATATGGATCCATCCCTCCTGATGTGGAGGAGAAGT 480	361 ACTTCCTAATTTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAAGTTACTGGCAAT 420	301 TTCGTACCTTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAG 360	241 CCATTGACGCCAACCTGGCCACGGACCCGCGGTTCCTCATCCTCCTGGGTTCTCCAAAGC 300	181 ACCTGGACTTCTTCACCCAGGACCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA 240	121 CGCTGGGTCCCCTCTCCCCTGGCGCCCTGCCCCCGACCTGCGCAAGCACAGGACGTCGTGG 180 121 CGCTGGGTCCCCTCTCCCCTGGCGCCCCTGCCCCGACCTGCCCCAAGCACAGGACGTCGTGG 180	61 AGATGCTGCCGCCCGAAGCCTGCGCTGCCGCCGCCGCTGATGCTGCTGCTCCTGGGGC 120	GGCGGGGGGAGCAGCCAGGTGA 	atch 100.0%; Score 1721; DB 6; Length 1721; al Similarity 100.0%; Pred. No. 0; 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Genetically modified cells and methods for expressing recombina heparanase and methods of purifying same Patent: US 634834-A 3 19-FEB-2002; Location/Qualifiers			AR194190 1721 bp DNA linear PAT 20 APR-2002 Sequence 3 from patent US 6348344.
RESULT 11 AR221285 LOCUS AR221285 1721 bp DNA linear PAT 26-SEP-2002 DEFINITION Sequence 1 from patent US 6426209.	Db 1681 CTGCTTGCATCTGAAATAAATATACTAGTCCTGACACTG 1721	1621	1561 TANAHARI GGIGGATGARICANAKUT TIGUUKUCI IIMAI GGAMAMAKUT UTUGGUUKAGAA 1 	1501 TANGACCTTIGGGACCTCAIGGATTACTTTCCAAATCTGCCCAACTCAATGGTCTAACTC	1441 TCACCAAGTACTTGCGGTTACCCTATCCTTTTCTAACAAGCAAG	⊢ ⊢	1321 TGGCAAGGTTCAAAGAAGAAGAAGAAGTTCGAGTATACCTTCATTGCACAAACA 1	1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA	1201	1141 CAGCIGGCITTATIGTIGGCIGGATAAATTIGGGCCIGTCAGCCCGAATIGGAATTIGGAGTIGG	1081 GGTTAGGAGAACAACTCTGCATATGGAGGCGGACGCCCTTGCTATCCGACACCTTTG	TTTCATCTGTGCAAAAAGTTTTCCAGGTGGTTGAGAGCACCAGGCCTGGCAAGAAGGTCT	QY 961 TGAATGGACGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTA 1020	AGAGCTTCCTGAAGGCTGGTGGAGAAGTGATTGATTCAGTTACATGGCATCACTACTATT	Qy 841 ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAGACGGCTAAGATGCTGA 900	OY 781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840	Qy 721 GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT 780

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Ayal-Hershkovitz,M., Pecker,I. and Yacoby-Zeevi, Genetically modified cells and methods for expre heparanase and methods of purifying same Patent: US 6426209-A 1 30-JUL-2002;

Location/Qualifiers

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Genetically modified cells and methods for expressing heparanase and methods of purifying same patent: US 6426209-A 3 30-JUL-2002;
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Miron, D.,

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RESULT 14 AR243204 AR243204 LOCUS DEFINITION Seq ACCESSION AR2 VERSION AR2 KEYWORDS SOUNCE Unk ORGANISM Unk REFERENCE 1 AUTHORS Benn TITLE Benn Heps	Qy 1621 c Db 1621 d Qy 1681 c Db 1681 c	Qy 1501 ; Db 1501 ; Qy 1561 ; Db 1561 ;	Qy 1381 Db 1381 Qy 1441 :	Db 1261 Qy 1321 Db 1321	1141 1201 1201	1021 1021 1081 1081	Oy 901 Db 901 Oy 961 Db 961
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REFERENCE 1 (bases 1 to 1721) AUTHORS Pecker,I., Vlodavsky,I., Friedman,Y. and Perets,T. TITLE Heparanase specific molecular probes and their use in research and medical applications JOURNAL Patent: US 6531129-A 1 11-MAR-2003; FEATURES Location/Qualifiers source /organism="unknown"	GI:29725129		Qy 1681 CTGCTTGCATCTGAAATATACTAGTCCTGACACTG 1721 Db 1681 CTGCTTGCATCTGAAAATATACTAGTCCTGACACTG 1721	1621 GTTCACTGGGCTTGCCAGCTTTCTCATATACTTTTTTTTGTG	1561 TAAAGATGGTGGATGATCAAACCTTTGCCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA	1501 TARGACCTTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC	QY 1441 TCACCAAGTACTTGCGGTTACCCTATCCTTTTTCTAACAAGCAAG	1381 CTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACG 	1321 TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACA	1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGCACCAAGGTGTTAA	1201 TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTTACCATTTAGTGGATGAAAACTTCGATC	1141 CAGCTGGCTTTATGTGGCTGGATAAATTGGGCTGTCAGCCCGAATGGAATAGAAGTGG	1081 GGTTAGGAGAACAAGCTCTGCATATGGAGGGGGGGGGGCCCCTTGCTATCCGACACCTTTG	1021 TTTCATCTGTGCAAAAGTTTTCCAGGTGGTTGAGAGCACCACGCCTGGCAAGAAGGTCT	OY 961 TGAATGGACGGACTGCTACCAGGGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTA 1020	901 AGAGCTTCCTGAAGGCTGGTGGAGAAGTGATTGATTCAGTTACATGGCATCACTACTATT 9

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ALIGNMENTS

REFERENCE AUTHORS REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CR604689 LOCUS DEFINITION ş ORIGIN COMMENT FEATURES TITLE JOURNAL REMARK Query Match Best Local Similarity Matches 1681; Conser JOURNAL source Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencasge : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencasge : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cNAN was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1685) Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization CR604689 1685 bp mRNA linear full-length cDNA clone CS0DI059YN15 of Placenta Cot Homo sapiens (human). Contact : Feng Liang Email : fliang@lifetech.com URL http://fulllength.invitrogen.com/ InVitroGen Corporat Genoscope. Faraday Avenue 2 (bases 1 to 1685) Unpublished Homo sapiens HTC; CNSLT cDNA. Homo sapiens (human) CR604689.1 GI:50485496 Conservative /organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9606" /clone="GODIO59YN15" /tissue_type="Placenta_Cot_2: /plasmid="pCMVSPORT_6" Cocation/Qualifiers 97.5%; 99.8%; 0 Score 1678.6; Pred. No. 0; 0; Mismatches 25-normalized' DB 4. ω •• Indels Length 1685; Corporation HTC 21-JUL-2004 25-normalized °, Gaps 1600 60 0

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RESULT 2
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mRNA linear of Placenta Cot

HTC 21-JUL-2004 25-normalized

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REMARK CR610536 Legislation CR610536 CR610536 CR610536 GI:50491343
HTC; CNSITE CDNA. Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1665)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Contact: Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue

2 (bases 1 to 1665)

REFERENCE AUTHORS TITLE

JOURNAL,

COMMENT

Direct Submission

AL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPQRT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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Location/Qualifiers

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/clone="CSODIOL987F04"
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/plasmid="pCMVSPORT_6"
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Mammalia; Eut
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                  Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
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AK040471.1 GI:26333764

HTC; CAP trapper.

Mus musculus (house mou
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S Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T., Kohori, F., Imotani, K., Colina, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki, Akahira, S., Muratatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Miramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Miramita, M., Tagawa, A., Takahashi, F., Takaki, A., Shiraki, T., Shirati, T., Miramatsu, M., and Hayashizaki, Y. Toya, T., Yasunishi, A., Miramita, M., Takaki, T., Tomaru, A., Toya, T., Yasunishi, A., Miramita, M., Takaki, T., Tomaru, A., Toya, T., Yasunishi, A., Miramita, M., Takaki, T., Tomaru, A., Toya, T., Yasunishi, A., Miramita, M., Takaki, T., Tomaru, A., Toya, T., Yasunishi, A., Miramita, M., Takaki, T., Tomaru, A., Toya, T., Yasunishi, A., Miramita, M., Takaki, M., Miramita, M., Takaki, M., Miramita, M., Miramita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1035)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31273967.
                                                                                                                                                                                                                          AL552151 Homo sapiens PLACENTA COT 25 NORMALIZED Homo sapiens cDNA clone CSODIO59YN15 3-PRIME, mRNA sequence.

AL552151 ARSON 
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                  Homo sapiens (human)
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For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO59CGO8NP1&c=2469.r. Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segrerf@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/clone="CSODI059YN15"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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/db_xref="taxon:9606"
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Length

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CCCTGATGTATTGGACATTTTTATTTCATCTGTGCAAAAAGTTTTTCCAGGTGGTTGAGAG
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TTTAGTGGATGAAAACTTCGATCCTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAA
                                                                                                           TTTAGTGGATGAAAACTTCGATCCTTTACCTGATTATTGGCTATCTCTTCTTGTTCAAGAA 1297
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Pred. No. 5.8e-252;
4; Mismatches 14;
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                                                                                                                                                          Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
Group Phase I & II Team
            The FANTOM Consortium and the RIKEN
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                                                  Nature 409,
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                                                                                              The RIKEN Genome Exploration Research
                                                                                 FANTOM Consortium.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AK087283.1 GI:26104170
HTC; CAP trapper.
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Direct Submission

AL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AL Nature 420, 563-573 (2002)
E 6 (bases 1 to 1962)
CE 6 (bases 1 to 1962)
RS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hara,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Myazaki,A., Murata,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsako,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
CCCACCGACCCGCGCTTCCTCACCTTCCTGGGCTCTCCAAGGCTCCGTGCTCTGGCTAGA
                                                                                                                                  GCCACGGACCCGCGGTTCCTCATCCTCCTGGGTTCTCCAAAGCTTCGTACCTTGGCCAGA
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/clone_Tib="RIKEN full-length enriched
/dev_stage="0 day neonate"
112 ___156
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/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="E030042C09"
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78.7%;
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Pred. No. 1.5e-246;
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TTACCCTATCCTTTTCTAACAAGCAAGTGGATAAATACCTTCTAAGACCTTTGGGACCT
                                    CAGGAAGGAGATCTAACTCTGTATGTCCTGAACCTCCATAATGTCACCAAGCACTTGAAG
                                                           AAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCATAACGTCACCACCAAGTACTTGCGG
                                                                                                           CCAGACAGGAGCAAACTCCGAGTGTATCTCCACTGCACTAACGTCTATCACCCACGATAT
                                                                                                                                                                                  CTCTCTCTTCTGTTCAAGAAACTGGTAGGTCCCAGGGTGTTACTGTCAAGAGTGAAAGGC
                                                                                                                                                                                                       CTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAATGGCAAGCGTGCAAGGT 1337
                                                                                                                                                                                                                                                                                  TTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACTTCGATCCTTTACCTGATTATTGG
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Feb 15, 2001 this sequence version replaced Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 1026)
Li, W.B., Gruber, C.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                            AGATGCTGCTGCGCTGGAAGCCTGCGCTGCCGCCGCTGATGCTGCTGCTCCTGGGGC
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                                                                                                                ACCTGGACTTCTTCACCCAGGAGCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA
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                                                                                 ACCTGGACTTCTTCACCCAGGAGCCGCTGCACCTGGTGAGCCCCTCGTTCCTGTCCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="Ist strand cDNa sprimed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNa was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized.
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7; Mismatches 6;
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Li, W.B., Gruber (C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31267106. Contact: Genoscope

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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand CDNA was primed with a NotI-oligo(dT) primer. Fi
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AL545270 AL545270.3 GI:45745753
EST.
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         GTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCTTCCAAGGGGTATAACATTTCTTGGG
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Local Similarity hes 916; Conserv
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                                                GTTCTAATGCTCAGTTGCTCCTGGACTACTGCTCCTTCCAAGGGGTATAACATTTCTTGGG
                                                                                                                 AGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCTCAG
                                                                                                                                       AGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTTGCAAACTGCTCAG
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/mol_type="mANA"

/db_xref="taxon:9606"

/db_xref="taxon:9606"

/clone="CSODIO28YPD4"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone="Ib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/clone="Ist strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR v

sites of the pCMVSPORT 6 vector. Library was normalized.
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TITLE
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                                                                                                                                                                                                               870;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1 (bases 1 to 1027)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31267068.
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                                                                                                                                                                                                                                Similarity
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                                                                                                                              ATATTTCATCAATGGTCGCAGTTAGGRGAAGATTTTATTCAATKGCATAAACTTCTAAGA
                                                                                                                                                 ATTTCATCAATGGGTCGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGA
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                                               AAGTCCACCTTCAAAAAWRAAAAACTCTATGGTCCTGATGTTTGGTCAGCCTCGAAGAAAG
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                                                                                                                                                                                                               Conservative
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/mol_type="mENA"
/db_xref="taxon:9606"
/clone="CSOD1028YF04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone=Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-olido(dT)
/note="Ist strand cDNA was primed with a NotI-olido(dT)
/note="Ist strand cDNA was primed with a NotI-olido cDNA was
grimer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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BX398409.2
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1066)

Li, W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30617572.

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2 rue Gaston Cremieux, CP 5706 - 91057 EURY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EURY cedex - FRANCE
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GABTON Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                            GI:46873668
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ACENTA COT 25-NORMALIZED Homo
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GGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGNGNNNNCCNNCNNNGCNCNNNCNC
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                                                                                    NTTNGKKGGGKGGTGGCGKKGGGGKGKKGGRGGKGKKGGTGGGCACCAAGGTGTTAAT
                                                                                                                ATTA----TTGGCTATCTCTTCTGTTCAAGAAAATTGGTGGGCACCAAGGTGTTAAT 1321
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                                                                                                                                                                                                       AAGTATTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACTTCGATCCTTTAACCTG
                                                                                                                                                                                                                                                                                         TTATGTGGCTGGATAAATTGGGCCTGTCAGCCCGAATGGGAATAGAAGTGGTGATGAGGC
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/clone="CSDD1058YI24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone lib="PLACENTA COT 25-NORMALIZED"
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqreføgenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX373611.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
On May 8, 2003 this sequence version replaced Contact: Genoscope
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           Conservative
                                                                                                    /tissue_type="PIACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                   /clone="CS0DI058YI24"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                            ACTTCCTAATTTTCGATCCCAAGAAGGAATCAACCTTTGAAGAGAGAAGTTACTGGCAAT
                                                                                                                                           TTCGTACCTTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTGGTGGCACCAAGACAG
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CTCAAGTCAACCAGGATATTTGCAAATATGGATCCATCCCTCCTGATGTGGAGGAGGAAGT
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                                                                                                                      TTCGTACCTTGGCCAGAGGCTTGTCTCCTGCGTACCTGAGGTTTTGGTGGCACCAAGACAG
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/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTVA-3', size-selected for average
insert size_2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Capt-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30340461"
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lab_host="DH10B TonA"
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Pred. No. 4.2e-199;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MCC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2393 row: a column: 18
High quality sequence stop: 710.
LCCation/Qualifiers
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1 (bases 1 to 924)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT 8343629 NIH_MGC_110
5', mENA sequence.
BQ691142
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EST.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:6250265"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/tissue_type="ductal carcinoma, cell line"
/clone_lib="MIH_MCC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5; adaptor: GGCACGAG(G). Library constructed by
of California, Berkeley) using ZAP-cDNA Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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sapiens cDNA clone IMAGE:6250265
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa;
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Query Match
Best Local Similarity
Matches 781; Conserv
BQ438834 907 b
AGENCOURT_7761619 NIH_MGC_70 H
5, mRNA sequence.
BQ438834
BQ438834.1 GI:21177910
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Pred. No. 6.2e-196;
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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plate: LLAM13218 row: b column: 01
High quality sequence stop: 616.
Location/Qualifiers
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AAGTGATTGATTCAGTTACATGGCATCACTAT-TTGAATGGACGGACTGCTACCA-G
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/mol type="mRN.9606"
/db xref="rtaxon.9606"
/clone="IMAGE:6017952"
/clone="IMAGE:6017952"
/lab host="DH108 (phage-resistant)"
/clone lib="WIH_MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: OTigo dT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryoča; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hom
1 (bases 1 to 708)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ775819
BQ775819.1 GI:21984295
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 FORWARD POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained Circa M. Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAGATTTTCTAAACCCTGATGTATTGGACATTTTTATTTCATCTG---TGCAAAAAGTT
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/(clone lib="WCI CGAP FHO"
//clone lib="WCI CGAP FHO"
//note="Grgan: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGAATCCGGC. The cell line was provided by Dr James Martin from University of Iowa
TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-H-FH0-bcg-a-07-0-UI"
/tissue_type="Human Chondrosarcoma Cell Line"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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Ś 밁

GmbH

Seq primer:

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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                    BX107633
                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                       ACCESSION
             TITLE
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 652)
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E. Radelof, U., Schneider, D. and Korn, B.
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                                                                                                                                                 BX107633.1 GI:27847484
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_SEQ=AGAATCCGGC"
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Pred. No. 1.
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                              Partsch, E.,
                                                              Hominidae;
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COMMENT
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Best Local Similarity
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 RZPD; IMAGP998B16561.

RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Human UnigeneSet - RZPDJ (RZPDLIB No. 972)

http://www.rzpd.de/CloneCards/cgi-
bin/ShowLib.pl.cgi/response7libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcencratum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
Fax: +49 30 32639 111
Fax: +49 30 32639 111
                                                                AAACACTGACAATCCAAGGTATAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCA 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                             AAACACTGACAATCCAAGGTATAAAAGAAGGAGATTTAACTCTGTATGCCATAAACCTCCA
                                                                                                          GTTAATGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
                                                                                                                                GTTAATGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGGTTCGAGTATACCTTCATTGCAC
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63.5	63.5	63.5	89.2	89.2	90.2	90.3	90.3	92.1	94.7	94.8	94.8	95.7	95.8	95.8	97.8	98.0	98.0	98.0	98.0	98.0	98.0	98.0	98.1	98.5
2396	2396	2396	1584	1584	1625	1625	1625	1593	1669	1669	1669	1673	1673	1673	1724	3726	3726	3726	3726	3726	3726	3726	1723	1713
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Adg88833 Mouse hpa	Aaa91113 Mouse hep		Aad63532 Chimeric	Abl40753 Chicken 8	_	Ado63820 Chimeric	Ado63819 Chimeric	Aaz11236 Human pre	Ad193950 Human G-c	Ade16011 G-coupled	Abz22816 Human hep	Ado63818 Human hep	Ado63817 Human hep	Ado63816 Human hep	Aah20940 Human hep	Adp25078 PRO polyp	Adq80253 Heparanas	Adn05073 Antipsori	Adn04901 Antipsori	Adk51968 Human ato	Add18951 Human dis	Aax86671 cDNA enco	Aax37260 Seq ID No	Aax37259 Human hep

ALIGNMENTS

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RESULT 1
AAX35648
Heparanase; hpa; modulator; heparin-binding growth factor; cellular response; cytokine; cell interaction; plasma lipoprotein; cellular susceptibility; infection; disintegration; neurodegenerative plaque; wound healing; angiogenesis; restenosis; athersclerosis; inflammation; neurodegenerative disease; neutralise;
                                              New human polynucleotide useful and inflammation.
                                                                                                                                         (INSI-) INSIGHT STRATEGY & MARKETING LTD. (HADA-) HADASIT MEDICAL RES SERVICES & DEV. (FRIE/) FRIEDMAN M M.
                                                                                                                                                                                         02-SEP-1997;
02-JUL-1998;
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                          plasma heparin; micrometastasis; autoimmune lesion; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding a human heparanase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX35648;
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                                                                                 P-PSDB; AAY02345.
                                                                                             WPI; 1999-302255/25.
                                                                                                                   Pecker I, Vlodavsky I,
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                                                                                                                     Feinstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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The specification describes a polypeptide having heparanase (hpa)

for treating angiogenesis, restenosis,

Claim 4; Fig 1; 63pp; English

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Query Match
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                                                                                                                                                                                                                            Sequence 1721
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                                                                                                                                                                                                                                                                                                                 CC The present sequence encodes a human protein with heparanase catalytic CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy, CC particularly in treating tunour, inflammation or autoimmunity. CC Particularly, the polynucleotide is useful in modulating the bioavailability of heparin-binding growth factors, cellular responses to CC particularly. The polynucleotide is useful in modulating the responses to CC interleukin (II)-8), cell interaction with plasma lipoproteins, cellular susceptibility to certain viral and some bacterial and protozoa CC infections, or disintegration of neurodegenerative plaques. The CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or radiation burns), and in the treatment of angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-CC Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral, or bacterial or protozoa infections
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Best Local S
Matches 1721
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                                                                                                                                                                                                                                            The present invention describes heparanase-specific molecular probes, cuseful for methods of detecting heparanase in situ. The probes and anti-
heparanase antibodies are used to detect or quantify the expression of heparanase, for diagnosis and monitoring of diseases (especially metastasis), for treatment of heparanase-associated diseases (e.g. tumours, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma, metastases) derived from liver, prostate, bladder, breast, ovary, cervix, colon, skin, intestine, stomach, uterus and panoreas, kidney disease, diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome, sepsis and inflammatory or autoimmune disease), for targeted drug delivery (e.g. of anticancer agents) and as research reagents. The present sequence encodes human heparanase, which is used in the
                                                                                                  Query Match
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Matches 1721; Conserv
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                             Page 82-84; 90pp;
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                                                                          TAAAGATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCCCAGGAA
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AAA91112 standard; DNA; 1721 ВP

20-APR-2001 (first entry)

Human heparanase, coding sequence fragment isolated from EST clone

RESULT 5
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AC AAA9
AC AAA9
AX Hepa
AX Hepa
KW Hepa
KW Hepa
KW Gene
KW Gene
KW Gene
XX Homc
AX Homc
XX Hom
XX Heparanase; hnhp1; wound healing; anglogenesis; restenosis; Scrape; atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease neurodegenerative disease; Creutzfeldt-Jakob disease; viral infectionen therapy; mouse; expressed sequence tag; ds. 's disease; infection;

sapiens.

WO200100643-A2

04-JAN-2001.

19-JUN-2000; 2000WO-IL000358

25-JUN-1999; 99US-0140801P.

INSIGHT STRATEGY & MARKETING

Ļ Michal I, Itzhaki Ξ

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WPI; 2001-137930/14.

New polynucleotides and polypeptides that are distantly homologous to

FEXSOCOCOCOXSXBA

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Query Match
Best Local Similarity 100
Matches 1721; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a human heparanase coding sequence clone, isolated from an EST clone. The invention relates to heparanase DNA and protein sequences. The heparanase DNA and protein sequences are useful i wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, pulmonary disease, neurodegenerative diseases (such as Scrape, Alzheimer's disease, and Creutzfeldt-Jakob diseases) or viral infections. The heparanase coding sequence is particularly useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1721 BP; 451 A; 413 C; 410 G; 447
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                                                              GGGAACTAGGCAATGAACCTAACAGTTTCCTTAAGAAGGCTGATATTTTCATCAATGGGT
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Best Local Similarity
Matches 1721; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to methods and compositions for inducing and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incision, necrosis, pressure wound, diabetic ulcer and to induce or accelerate angiogenesis. The present sequence is human hpa cDNA.
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01-MAR-1999; 99US-00258892.

06-FEB-2001; 2001US-00776874.

05-SEP-2001; 2001WG-IL000830.

19-NOV-2001; 2001US-00988113.
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) YACOBY-ZEEVI
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                                                       3; gene; heparanase-dependent cancer;
inflammation; chromosome 4.
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CC polynucleotide or a polynucleotide analogue of at least 10 bases being comprising a comprisite and in vivo, under physiological conditions, with a portion of catalytic activity. Also included are a method of in vivo downregulating conditions and in vivo catalytic activity. Also included are a method of in vivo downregulating conditions and in vivo downregulating conditions and in vivo downregulating conficted by heparanase activity, comprising administering the ASO in vivo), a method conficted by heparanase activity, comprising administering and an antisense nucleic acid construct (comprising a promoter conficted by heparanase activity, comprising administering the ASO and a carrier, an antisense nucleic acid construct (comprising a promoter condered by heparanase activity, comprising a promoter condered by sequence of at least 10 bases being hybridisable in vivo, condered by forming and conditions, with a polynucleotide strand encoding a conditions of a construct (comprising a method of in vivo comprising the antisense nucleic acid construct), a pharmaceutical composition comprising the antisense nucleic acid construct (comprising a method of in vivo comprising the antisense nucleic acid construct and a carrier, and an analogue of at least 10 bases being hybridisable in vivo the comprising the antisense nucleic acid construct and a carrier, and an analogue of at least 10 bases being hybridisable in vivo, under construct to a polynucleotide strand being construct and a carrier, and an analogue of at least 10 bases being hybridisable in vivo, under construct of a polynucleotide strand being construct and a carrier, and an analogue of at least 10 bases being hybridisable in vivo, under construct and a carrier, and an analogue of at least 10 bases being hybridisable in vivo, under construct of a polynucleotide strand being construct and a carrier, and an analogue of a least 10 bases being hybridisable in vivo, under construct of the construct o
Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
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01-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense oligonucleotide hybridizable with a polynucleotide encoding a polypeptide with heparanase activity, useful for treating diseases such as cancer and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID NO 11;
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                                                    present sequence is a human heparanase cDNA.
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01-MAR-1999;
08-NOV-1999;
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                                                                        New antisense oligonucleotide hybridizable with a polypeptide with heparanase activity, useful fas cancer and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ss; heparanase; gene; heparanase-dependent cancer; autoimmune reaction; inflammation; chromosome 4.
                                        Claim
                                                                                                                                                                                                                         (INSI-)
(HADA-)
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                                                                                                                                                                                  Vlodavsky I,
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99US-00258892.
99US-00435739.
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/*tag= a
/note= "Claimed in claim
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-91 TCAAGAACAGCACCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCAAACTGCT	481	481 TACGGTTTGGAATGGGGGT	361 421		241		121	61	6 1 ,		SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Oth	CC as heparanase-dependent cancer, cancer, autoimmune react cc inflammation. The gene for human heparanase is located of the present sequence is a human heparanase cDNA.	CC heparanase catalytic activity. The methods and composity of present invention are useful for the prevention and/or of diseases or conditions associated with the prevention and/or of the prevent	CC physiological conditions, with a portion of a polynucle CC characterised by forming at least a portion of an untraince (ITYPE) for a condition of an untraince of the condition of the condition of the conditio	CC comprising the antisense nucleic acid construct and a c comprising the antisense nucleic acid construct and a c c antisense oligonucleotide comprising a polynucleotide o c analogue of at least 10 becomes and polynucleotide o	CC under physiological conditions, with a polynucleotide s CC polypeptide having heparanase catalytic activity), a me CC downregulating heparanase activity (comprising administ CC artisease works.	CC the subject), a pharmaceutical composition comprising to carrier, an antisense nucleic acid construct (comprising to sequence and a polynucleotide sequence directing the sy CC antisense RNA sequence of the system of the sys	CC heparanase activity (comprising administering the ASO of treating a subject suffering from a pathological core (characterised by heparanase activity comprising from a pathological core.)	CC polynucleotide or a polynucleotide analogue of at least 10 bases being CC hybridisable in vivo, under physiological conditions, with a portion of CC a polynucleotide strand encoding a polypeptide having heparanase
600 QY 1621 600 Db 1621	540 CY 1561 540 Db 1561	TGGAGGAGAAGT 480	420 Oy 1441 420 Db 1441	360 Qy 1381 360 Db 1381	GGTTCTCCAAAGC 300 Qy 1321 GGTTCTCCAAAGC 300 Db 1321	240	\cagacgTcgTcg 180	OY	GCCAGGTGAGCCCA 60	0; Db	рь	ase activity, such Db 901 tion and On chromosome 4. Qy 961	treatment of Db 841		mposition Qy 781 carrier, and an Db 781 or a polynucleotide	B 5	g 25	O D	γQ
1	TAAAGATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620 	TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCTAACTC 1560		14 14	TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACAAACA 1380 		TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAAACTTCGATC 1 					AGAGCTTCCTGAAGGCTGGTGGAGAGAGTGATTCAGTTACATGGCATCACTACTATT TGAATGGACGGCTGCTACCAGGAAGAGTTTCTAGATTCAGTTACATGGCATCACTACTATT TGAATGGACGGCTGCTACCAGGAAGAGTTTTCTAAAACCCTACTATT	ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAAACACGGCTAAGATGCTGAAGACGTCTGAAGGCTTGCTGAAGGCTTGGTGGAAGAAGTGATTGAT	ATGCAAAACTCTATGGTCCTGATGTTGGTCAGCCTCGAAGAAACTCTATGGTCTGATGTTGGTCAGCCTCGAAGAAACTGGCTAA	CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA				

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01-MAR-1999;
06-FEB-2001;
19-NOV-2001;
                                                                  The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, the used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases, atherosclerosis and pulmonary disorders. The present sequence is human hpa cDNA used in the exemplification of the invention.
                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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DB; ADM48716.
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VLODAVSKY I
METZGER S.
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2001US-00776874.
2001US-00988113.
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disease; atherosclerosis; pulmonary disorder; hpa;
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Best Local Similarity
Matches 1721; Conserv
                                                                                                                                                                                         The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynuclectide sequence, including a promoter active in tissues of the non-human, a region encoding a human are operably linked in the exogenous polynucleotide such that human are operably linked in the exogenous polynucleotide such that human human animal. The methods and compositions of the cells of the non-useful for the production of transgenic animals expressing heparanase, the used as models for human diseases such as cancers, viral infection, restenosis, neurodegenerative diseases such as cancers, viral infection, disorders. The present sequence is human hpa cDNA used in the exemplification of the invention.
                                                                                                                                                                          Sequence
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01-MAR-1999;
06-FEB-2001;
19-NOV-2001;
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l T, Goldshmidt O;
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중 유 ð 음 성 밁 ð 밁 ঠ 뭥 8 유

The specification describes a polypeptide having heparanase (hpa) activity. The recombinant protein is used as a modulator of heparin-binding growth factors cellular responses to heparin-binding growth factors and cytckines, cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoal and bacterial infections or disinteraction of neurodegenerative plaques. Heparanase may be useful for conditions such as wound healing, angiogenesis, restenosis, athersclerosis, inflammation, neurodegenerative diseases, and viral infections. Mammalian heparanase can be used to neutralize plasma heparin, and anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, antoimmune lesions, ar renal failure in biopsy specimens, plasma samples, and body fluids. The

for

Claim 4; Page 64-65; 63pp;

English

Sequence 1899 BP; 495 A; 433

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510 G;

461 H .. 0 U;

0 Other;

present sequence

encodes

human heparanase

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ARASJULT 12
ARASJ5650
ID ARASJ5650
XX ARASJ5
XX Hepax
XX Hepax
XX Plasm
XX Plasm
XX WO991
XX WO991
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02-JUL-1998;
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                                                                       The present invention relates to methods and compositions for inducing and/or accelerating wound healing via the catalytic activity of heparanase. The invention is used to induce or accelerate a healing process, particularly of an ulcer, burn, laceration, surgical incision necrosis, pressure wound, diabetic ulcer and to induce or accelerate angiogenesis. The present sequence is human SK-hepl cDNA.
                                                    Sequence 1899
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06-FBB-2001; 2001US-00776874.
05-SEP-2001; 2001US-1000830.
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05-SEP-2001;
19-NOV-2001;
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            TACGGTTGGAATGGCCCTACCAGGAGCAATTGCTACTCCGAGAACACTACCAGAAAAAGT
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                                                                                                                                                                                                                                                       CGCTGGGTCCCCTCTCCCCTGGCGCCCTGCCCCGACCTGCGCAAGCACAGGACGTCGTGG
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nilarity 99.9%;
Conservative
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99US-00258892.
2001US-00776874.
2001WG-UL000830.
2001US-00988113.
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Pred. No. 0;
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1561 TAAAGATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCCAGGAA 1620 	501 TAAGACCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTC	441 TCACCAAGTA 619 TCACCAAGTA	81 CTGACAATCCA 59 CTGACAATCCA	321 TGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACCTTCATTGCACA 	1261 CTTTACCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGTGTTAA 1320 	201 TGATGAGGCAAGTATTCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACTTCGATC 12 	1141 CAGCTGGCTTTATGTGGCTGGATAAATTGGGCCTGTCAGCCCGAATGGGAATAGAAGTGG 1200 	1081 GGTTAGGAGAAACAAGCTCTGCATATGGAGGCGGAGCGCCCTTGCTATCCGACACCTTTG 1140	1021 TITCATCTGTGCAAAAGTTTTTCCAGGTGGTTGAGAGCACCAGGCCTGGCAAGAAGGTCT 1080 	GAAGATTITCTAAACCCTGATGTATTGGACATTTTTA 1 	01 AGAGCTTCCTGA# 	141 ATGCAAA 19 ATGCAAA	781 CGCAGTTAGGAGAAGATTATATTCAATTGCATAAACTTCTAAGAAAGTCCACCTTCAAAA 840 	99 96	61 ACAGTTCTAATG 39 ACAGTTCTAATG	601 CAGGACTGGACTTGATCTTTGGCCTAAATGCGTTAATAAGAACAGCAGATTTTGCAGTGGA 660 	1 TCAAGAACAGCACCTACTC

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1859 CTGCTTGCATCTGAAAATAAAATATACTAGTCCTGACACTG 1899	1681 CTGCTTGCATCTGAAAATAAAATATACTAGTCCTGACACTG 1721	1799 GTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTGTGATAAGAAATGCCAAAGTTG 1858	1621 GTTCACTGGGCTTGCCAGCTTTCTCATATAGTTTTTTTTGTGATAAGAAATGCCAAAGTTG 1680

Search completed: March 2, 2005, 00:46:13 Job time: 896 secs